

#4

ATGTCCTCGCGCCGTCTCCGGGG	24
M S S A P S P G	
25 ACTGGTTCGCCTCCATCTCCACCATCAAACCTCCACAAACCACCACTCCTCCAGCTTCC	84
T G S P P S P P S N* S T T T T P P P A S	
85 GCTCCTCCTCCCACACACCTTCTTCTCCTCCGCCATCCACTATTCCGACATCTCCT	144
A P P P T T P S S P P P P S T I P T S P	
145 CCTCCTTCTTCTCGCTCTACACCTTCTGCTCCTCCATCTCCACCAACTCCATCTACG	204
P P S S R S T P S A P P P P S P P T P S T	
205 CCGGGATCTCCACCTCCTCTTCCTCAGCCGTCTCCACCCGCTCCAACACTACGCCGGATCT	264
P G S P P P L P Q P S P P A P T T P G S	
265 CCACCCGCACCTGTTACTCCTCCTACTCGAAACCCCTCCACCTTCAGTCCCAGGACCACCG	324
P P A P V T P P T R N P P P P S V P G P P	
325 TCCAATCCTTCACGCGAAGGAGGATCTCCTCGACCTCCATCTTCTCCCTGCCCGCTCT	384
S N P S R E G G S P R P P P S S P S P P S	
385 CCTTCTTCCGACGGTTATCAACAGGAG <u>TGGTGGTGG</u> ATGCCATCGGAGGAGTCGCT	444
P S S D G L S T G V V V G I A I G G V A	
445 <u>CTGCTTGTGATAGTGACTCTGATTGTCCTCTGT</u> AAGAAGAAACGACGGAGAGACGAA	504
L L V I V T L I C L L C K K K R R R R D E	
505 GAAGATGCTTACTATGTTCCCTCGCCACCTCCTGGTCCAAAGCCGGAGGACCTTAC	564
E D A Y Y V P P P P P G P K A G G P Y	
565 GGTGGACAGCAGCAACAATGGCGGAAACAAACGCAACACCACCGTCAGATCATGTCGTG	624
G G Q Q Q W R Q Q N A T P P S D H V V	
625 ACGTCACTACCACCACCACTAAGGCTCCATCTCCACCACGGCAACCTCCTCACCTCCA	684
T S L P P P P K A P S P P R Q P P P P P P	
685 CCACCGCCTTCATGAGCAGCAGCGGGCTCCGACTACTCGGACCGTCCAGTTCTCCT	744
P P P F M S S S G G S D Y S D R P V L P	

FIG. 1A(1)

745 CCACCGTCTCCAGGGCTTGTGTTAGGCTCTCCAAAAGCACTTCACATACGAGGAGCTA 804
 P P S P G L V L G F S K S T F T Y E E L
 805 GCTAGAGGCCACCAATGGTTCTCCGAGGCGAACCTGTTAGGACAAGGCAGGTTAGCTAC 864
 A R A T N ^IG F S E A N L L G Q G G F G Y
 865 GTGCACAAAGGTGTGTTGCCTAGTGGAAAGAAGTTGCTGTGAAGCAGTTGAAAGTTGGG 924
 V H K G V L P S ^{II}G K E V A V K Q L K V G
 925 AGTGGTCAGGGAGAGAGGGAGTTCAAGGCAGAGGTTGAGATCATCAGCAGAGTTCAACCAC 984
 S G ^{III}Q G E R E F Q A E V E I I S R V ^{IV}H H
 985 AGGCATCTGGTGTCTTGGTTATTGCATGCCGGTGCCTAAAGATTGCTTGTCTAT 1044
 R H L V S L V G Y C I A ^VG A K R L L V Y
 1045 GAGTTGTTCTAACACAATCTCGAGCTTCACCTCCATGGCGAGGGACGGCCTACAATG 1104
 E F V P N N N L E L H L H G E G R ^{VI}P T M
 1105 GAATGGAGCACCAGATTGAAGATTGCTCTGGATCTGCTAAAGGACTTCTTATCTTCAT 1164
 E W S T R L K I A L G S A K G L S Y L H
 1165 GAAGATTGCAATCCTAAAATCATTACCGTGATATCAAGGCTTCAAACATATTGATAGAT 1224
 E D C N P K I I H R D I K A S N I L I D
 1225 TTCAAGTTGAAGCTAAGGTTGCTGATTTGGTCTTGCTAAGATTGCTTCTGATAACAAAC 1284
 F K F ^{VII}E A K V A D F G L A K I A S D T N
 1285 ACGCATGTATCAACACGTGTGATGGAACCTTGGTACTTGGCTCCGAATACGCTGCA 1344
 T H V ^{VIII}S T R V M G T F G Y L A P F Y ^{IX}A A
 1345 AGCGGAAAGCTCACGGAGAAGTCTGACGTTCTCATTTGGCGTTGTGCTTGGAGCTC 1404
 S G K L T E K S D V F S F G V V L L E L
 1405 ATTACTGGACGTGACCCGTTGATGCCAACATGTCTATGTAGATGACAGCTTAGTTGAC 1464
 I T G R R P V D A N N ^XV Y V D D S L V D
 1465 TGGGCACGACCATTGCTTAACCGAGCATCTGAGCAAGGAGACTTGAGGGTTAGCTGAT 1524
 W A R P L L N R A S E Q G D F E G L A D

FIG. 1A(2)

1525 GCAAAGATGAATAATGGGTATGACAGAGAGGAGATGGCTCGCATGGTTGCTTGCTGCG 1584
 A K M N N G Y D R E ^{XI} E M A R M V A C A A
 1585 GCTTGTGTTGCCATTAGCTCGCCGAGACCTCGCATGAGCCAGATTGTGCGTGCCTTA 1644
 A C V R H S A R R P R M S Q I V R A L
 1645 GAAGGAAATGTATCACTGTCAGATCTAACGAAGGGATGAGACCAGGTCAAAGCAATGTA 1704
 E G N* V S L S D L N E G M R P G Q S N V
 1705 TACAGCTCATACGGAGGAAGCACCGATTATGACTCGAGCCAGTACAATGAAGACATGAAG 1764
 Y S S Y G G S T D Y D S S Q Y N E D M K
 1765 AAGTTTAGGAAAATGGCACTTGGAACTCAAGAGTACAACGCCACGGGTGAGTACAGTAAT 1824
 K F R K M A L G T Q E Y N* A T G E Y S N
 1825 CCGACCAGTGACTATGGACTGTACCCGTCTGGTTCAAGCAGCGAGGGCAAACACACGC 1884
 P T S D Y G L Y P S G S S S E G Q T T R
 1885 GAAATGGAGATGGGAAGATTAAGAGAACCGGTCAAGGGTTATAGTGGACCTCTCTTAA 1944
 E M E M G K I K R T G Q G Y S G P S L *

FIG. 1A(3)

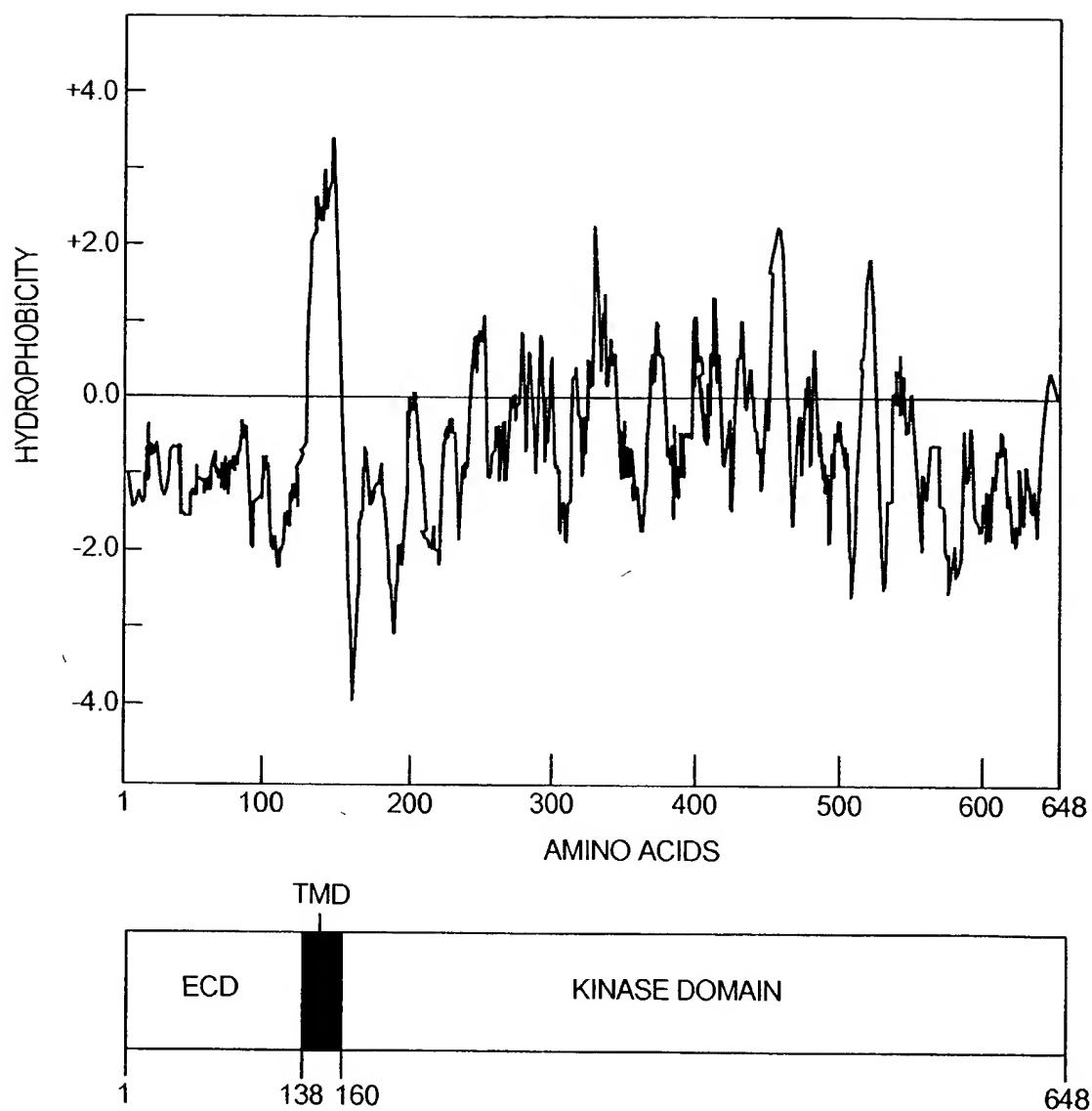


FIG. 1B

-95 <i>ttaactctggtctccgtgtctcctcttctcctgctgcttcctttaaacactcttt</i> -36 -35 <i>catttgccctttttagatccaaagaaggcagac</i> ATGTCCTCGGCGCCGTCTCCGGGG 25 ACTGGTTGCCTCCATCTCCACCATCAAACCTCCACAAACCACCACTCCTCCAGCTTCC 84 T G S P P S P P S N* S T T T T P P P A S 85 GCTCCTCCTCCCACACACACCTCTTCTCCTCCGCCATCCACTATTCCGACATCTCCT 144 A P P P T T P S S P P P P S T I P T S P 145 CCTCCTTCTTCTCGCTCTACACCTCTGCTCCTCCATCTCCACCAACTCCATCTACG 204 P P S S R S T P S A P P P S P P T P S T 205 CCGGGATCTCCACCTCCTCTTCAGCCGTCTCCACCCGCTCCAACCTACGCCGGATCT 264 P G S P P P L P Q P S P P A P T T P G S 265 CCACCCGACCTGTTACTCCTCCTACTCGAAACCCCTCCACCTTCAGTCCCAGGACCACG 324 P P A P V T P P T R N P P P S V P G P P 325 TCCAATCCTTCACGCGAAGGAGGATCTCCTCGACCTCCATCTCCTCGCCCGCTCT 384 S N P S R E G G S P R P P S S P S P P S 385 CCTTCTCCGACGGTTATCAACAGGAG <u>TGGTGGATCGCCATCGGAGGAGTCGCT</u> 444 P S S D G L S T G V V V G I A I G G V A 445 <u>CTGCTTGTGATAGTGACTCTGATTGCTCCTCTGTAAGAAGAAACGACGGAGAGACGAA</u> 504 L L V I V T L I C L L C K K K R R R D E 505 GAAGATGCTTACTATGTTCCCTCGCCACCTCCTCTGGTCCAAAGCCGGAGGACCTTAC 564 E D A Y Y V P P P P P G P K A G G P Y 565 GGTGGACAGCAGCAACAATGGCGGAACAAACGCAACACCACCGTCAGATCATGTCGTG 624 G G Q Q Q Q W R Q Q N A T P P S D H V V 625 ACGTCACTACCACCACCACTAAGGCTCCATCTCCACCACGGCAACCTCCTCACCTCCA 684 T S L P P P P K A P S P P R Q P P P P P	-95 <i>ttaactctggtctccgtgtctcctcttctcctgctgcttcctttaaacactcttt</i> -36 -35 <i>catttgccctttttagatccaaagaaggcagac</i> ATGTCCTCGGCGCCGTCTCCGGGG 25 ACTGGTTGCCTCCATCTCCACCATCAAACCTCCACAAACCACCACTCCTCCAGCTTCC 84 T G S P P S P P S N* S T T T T P P P A S 85 GCTCCTCCTCCCACACACACCTCTTCTCCTCCGCCATCCACTATTCCGACATCTCCT 144 A P P P T T P S S P P P P S T I P T S P 145 CCTCCTTCTTCTCGCTCTACACCTCTGCTCCTCCATCTCCACCAACTCCATCTACG 204 P P S S R S T P S A P P P S P P T P S T 205 CCGGGATCTCCACCTCCTCTTCAGCCGTCTCCACCCGCTCCAACCTACGCCGGATCT 264 P G S P P P L P Q P S P P A P T T P G S 265 CCACCCGACCTGTTACTCCTCCTACTCGAAACCCCTCCACCTTCAGTCCCAGGACCACG 324 P P A P V T P P T R N P P P S V P G P P 325 TCCAATCCTTCACGCGAAGGAGGATCTCCTCGACCTCCATCTCCTCGCCCGCTCT 384 S N P S R E G G S P R P P S S P S P P S 385 CCTTCTCCGACGGTTATCAACAGGAG <u>TGGTGGATCGCCATCGGAGGAGTCGCT</u> 444 P S S D G L S T G V V V G I A I G G V A 445 <u>CTGCTTGTGATAGTGACTCTGATTGCTCCTCTGTAAGAAGAAACGACGGAGAGACGAA</u> 504 L L V I V T L I C L L C K K K R R R D E 505 GAAGATGCTTACTATGTTCCCTCGCCACCTCCTCTGGTCCAAAGCCGGAGGACCTTAC 564 E D A Y Y V P P P P P G P K A G G P Y 565 GGTGGACAGCAGCAACAATGGCGGAACAAACGCAACACCACCGTCAGATCATGTCGTG 624 G G Q Q Q Q W R Q Q N A T P P S D H V V 625 ACGTCACTACCACCACCACTAAGGCTCCATCTCCACCACGGCAACCTCCTCACCTCCA 684 T S L P P P P K A P S P P R Q P P P P P
---	---

FIG. 1C(1)

685 CCACCGCCTTCATGAGCAGCAGCGCGGCTCCGACTACTCGGACCGTCCAGTTCTCCT 744
 P P P F M S S S G G S D Y S D R P V L P
 745 CCACCGTCTCCAGGGCTTGTGTTAGGCTTCTCCAAAAGCACTTCACATACGAGGAGCTA 804
 P P S P G L V L G F S K S T F T Y E E L
 805 GCTAGAGGCCACCAATGGTTCTCCGAGGCGAACTGTTAGGACAAGGCAGGTTCGGTTAC 864
 A R A T N ^IG F S E A N L L G Q G G F G Y
 865 GTGCACAAAGGTGTGTTGCCTAGTGGAAAGAAGTTGCTGTGAAGCAGTTGAAAGTTGGG 924
 V H K G V L P S ^{II}G K E V A V K Q L K V G
 925 AGTGGTCAGGGAGAGAGGGAGTTCAAGGCAGAGGTTGAGATCATCAGCAGAGTTCACAC 984
 S G ^{III}Q G E R E F Q A E V E I I S R V ^{IV}H H
 985 AGGCATCTGGTGTCTTGTGTTATTGCATGCCGGTGCCAAAGATTGCTTGTCTAT 1044
 R H L V S L V G Y C I A ^VG A K R L L V Y
 1045 GAGTTTGTCTAACAAACATCTGAGCTTCACCTCCATGGCGAGGGACGGCCTACAATG 1104
 E F V P N N N L E L H L H G E G R ^{VI}P T M
 1105 GAATGGAGCACCAGATTGAAGATTGCTCTGGATCTGCTAAAGGACTTCTTATCTTCAT 1164
 E W S T R L K I A L G S A K G L S Y L H
 1165 GAAGATTGCAATCTAAATCATTACCGTGATATCAAGGCTTCAAACATATTGATAGAT 1224
 E D C N P K I I H R D I K A S N I L I D
 1225 TTCAAGTTGAAGCTAACAGTTGCTGATTTGGTCTTGTAAAGATTGCTTCTGATAACAAAC 1284
 F K F ^{VII}E A K V A D F G L A K I A S D T N
 1285 ACGCATGTATCAACACGTGTGATGGAACCTTGGGTACTTGGCTCCGGAATACGCTGCA 1344
 T H V ^{VIII}S T R V M G T F G Y L A P E Y ^{IX}A A
 1345 AGCGGAAAGCTCACGGAGAAGTCTGACGTTCTCATTGGCGTTGTGCTTTGGAGCTC 1404
 S G K L T E K S D V F S F G V V L L E L

FIG. 1C(2)

1405 ATTACTGGACGTCGACCCGTTGATGCCAACAAATGTCTATGTAGATGACAGCTTAGTTGAC 1464
I T G R R P V D A N N X V Y V D D S L V D
 1465 TGGGCACGACCATTGCTTAACCGAGCATCTGAGCAAGGAGACTTGAGGGTTAGCTGAT 1524
W A R P L L N R A S E Q G D F E G L A D
 1525 GCAAAGATGAATAATGGGTATGACAGAGAGGAGATGGCTCGCATGGTTGCTGTGCG 1584
A K M N N G Y D R E X^I E M A R M V A C A A
 1585 GCTTGTGTTGCCATTCAAGCTCGCCAGACCTCGCATGAGCCAGATTGTGCGTGCCTTA 1644
A C V R M S A R R R P R M S Q I V R A L
 1645 GAAGGAAATGTATCACTGTCAGATCTAACGAAGGGATGAGACCAGGTCAAAGCAATGTA 1704
E G N* V S L S D L N E G M R P G Q S N V
 1705 TACAGCTCATACGGAGGAAGCACCGATTATGACTCGAGCCAGTACAATGAAGACATGAAG 1764
Y S S Y G G S T D Y D S S Q Y N E D M K
 1765 AAGTTTAGGAAATGGCACTTGGAACTCAAGAGTACAACGCCACGGGTGAGTACAGTAAT 1824
K F R K M A L G T Q E Y N* A T G E Y S N
 1825 CCGACCAGTGAATGGACTATGGACTGTACCCGTCTGGTTCAAGCAGCGAGGGCCAAACCACACGC 1884
P T S D Y G L Y P S G S S S E G Q T T R
 1885 GAAATGGAGATGGGAAGATTAAGAGAACCGGTCAAGGGTTATAGTGGACCTCTCTTAA 1944
E M E M G K I K R T G Q G Y S G P S L *
 1945 accagatgggagagaaattgaagggtgtttttcattttttaaaactgtaaagata 2004
 2005 tgagaaaattgccttactctaattaaaaccactacgatataaggtaataacgtttga 2064
 2065 attggtttttaaaaaaaaaaaaaaaaaaaaaaa 2093

FIG. 1C(3)

10	20	30	40	50	60
TTAACTCTCT	GGTCTCCGTG	TCTCCTCTCT	TCTCCTGCTG	CTTCCTTTTA	ACACTCTCTT
70	80	90	100	110	120
CATTGCGCTT	TTTGATTTAG	ATCCAAAGAA	GCAGACATGT	CCTCGGCGCC	GTCTCCGGGG
130	140	150	160	170	180
ACTGGTTCGC	CTCCATCTCC	ACCATCAAAC	TCCACAAACCA	CCACTCCTCC	TCCAGCTTCC
190	200	210	220	230	240
GCTCCTCCTC	CCACCAACACC	TTCTTCTCCT	CCGCCGCCAT	CCACTATTCC	GACATCTCCT
250	260	270	280	290	300
CCTCCTTCTT	CTCGCTCTAC	ACCTTCTGCT	CCTCCTCCAT	CTCCACCAAC	TCCATCTACG
310	320	330	340	350	360
CCGGGATCTC	CACCTCCTCT	TCCTCAGCCG	TCTCCACCCG	CTCCAACCTAC	GCCCGGATCT
370	380	390	400	410	420
CCACCCGCAC	CTGTTACTCC	TCCTACTCGA	AACCCTCCAC	CTTCAGTCCC	AGGACCACCG
430	440	450	460	470	480
TCCAATCCTT	CACGCGAAGG	AGGATCTCCT	CGACCTCCAT	CTTCTCCCTC	GCCGCCGTCT
490	500	510	520	530	540
CCTTCTTCCG	ACGGTTTATC	AACAGGAGTG	GTGGTGGGAA	TCGCCATCGG	AGGAGTCGCT
550	560	570	580	590	600
CTGCTTGTGA	TAGTGACTCT	GATTTGTCTC	CTCTGTAAGA	AGAAACGACG	GAGAGACGAA
610	620	630	640	650	660
GAAGATGCTT	ACTATGTTCC	TCCGCCACCT	CCTCCTGGTC	CCAAAGCCGG	AGGACCTTAC
670	680	690	700	710	720
GGTGGACAGC	AGCAACAATG	GCGGCAACAA	AACGCAACAC	CACCGTCAGA	TCATGTCGTG
730	740	750	760	770	780
ACGTCACTAC	CACCACCACC	TAAGGCTCCA	TCTCCACCAC	GGCAACCTCC	TCCACCTCCA
790	800	810	820	830	840
CCACCGCCTT	TCATGAGCAG	CAGCGGCGGC	TCCGACTACT	CGGACCGTCC	AGTTCTTCCT
850	860	870	880	890	900
CCACCGTCTC	CAGGGCTTGT	GTTAGGCTTC	TCCAAAAGCA	CTTTCACATA	CGAGGAGCTA
910	920	930	940	950	960
GCTAGAGCCA	CCAATGGTTT	CTCCGAGGCG	AACTTGTAG	GACAAGGCGG	GTTCGGTTAC
970	980	990	1000	1010	1020
GTGCACAAAG	GTGTGTTGCC	TAGTGGAAA	GAAGTTGCTG	TGAAGCAGTT	GAAAGTTGGG
1030	1040	1050	1060	1070	1080
AGTGGTCAGG	GAGAGAGGGA	GTTCAGGCA	GAGGTTGAGA	TCATCAGCAG	AGTTCACCAAC
1090	1100	1110	1120	1130	1140
AGGCATCTGG	TGTCTCTTGT	TGGTTATTGC	ATCGCCGGTG	CCAAAAGATT	GCTTGTCTAT
1150	1160	1170	1180	1190	1200
GAGTTTGTTC	CTAACAAACAA	TCTCGAGCTT	CACCTCCATG	GCGAGGGACG	GCCTACAATG
1210	1220	1230	1240	1250	1260
GAATGGAGCA	CCAGATTGAA	GATTGCTCTT	GGATCTGCTA	AAGGACTTTC	TTATCTTCAT
1270	1280	1290	1300	1310	1320
GAAGATTGCA	ATCCTAAAAT	CATTCAACCGT	GATATCAAGG	CTTCAAACAT	ATTGATAGAT
1330	1340	1350	1360	1370	1380
TTCAAGTTG	AAGCTAAGGT	TGCTGATTTT	GGTCTTGCTA	AGATTGCTTC	TGATACAAAC
1390	1400	1410	1420	1430	1440
ACGCATGTAT	CAACACGTGT	GATGGGAACC	TTTGGGTACT	TGGCTCCCGGA	ATACGCTGCA
1450	1460	1470	1480	1490	1500
AGCGGAAAGC	TCACGGAGAA	GTCTGACGTT	TTCTCATTG	GCGTTGTGCT	TTTGGAGCTC
1510	1520	1530	1540	1550	1560

FIG. 1D(1)

ATTACTGGAC	GTCGACCCGT	TGATGCCAAC	AATGTCTATG	TAGATGACAG	CTTAGTTGAC
1570	1580	1590	1600	1610	1620
TGGGCACGAC	CATTGCTTAA	CCGAGCATCT	GAGCAAGGAG	ACTTTGAGGG	TTTAGCTGAT
1630	1640	1650	1660	1670	1680
GCAAAGATGA	ATAATGGGT	TGACAGAGAG	GAGATGGCTC	GCATGGTTGC	TTGTGCTGCG
1690	1700	1710	1720	1730	1740
GCTTGTGTT	GCCATTCA	TCGCCGCAGA	CCTCGCATGA	GCCAGATTGT	GCGTGCCTTA
1750	1760	1770	1780	1790	1800
GAAGGAAATG	TATCACTGTC	AGATCTTAAC	GAAGGGATGA	GACCAGGTCA	AAGCAATGTA
1810	1820	1830	1840	1850	1860
TACAGCTCAT	ACGGAGGAAG	CACCGATTAT	GACTCGAGCC	AGTACAATGA	AGACATGAAG
1870	1880	1890	1900	1910	1920
AAGTTT AG GA	AAATGGCACT	TGGA ACT CAA	GAGTACAACG	CCACGGGTGA	GTACAGTAAT
1930	1940	1950	1960	1970	1980
CCGACCAGTG	ACTATGGACT	GTACCCGTCT	GGTCAAGCA	GCGAGGGCCA	AACCACACGC
1990	2000	2010	2020	2030	2040
GAAATGGAGA	TGGGGAAAGAT	TAAGAGAAC	GGTCAGGGTT	ATAGTGGACC	TTCTCTTAA
2050	2060	2070	2080	2090	2100
ACCAGATGGG	AGAGAAATTG	AAGGGTGT	TTTCATTATT	TTTTAAAAC	TGTAAAGATA
2110	2120	2130	2140	2150	2160
TGAGAAAATT	GCCTTACTCT	AATTAAAACC	ACTACGATAT	AAGGTTATAA	TACGTTTGA
2170	2180	2190	2200	2210	2220
ATTGGTTTTT	AAAAAAAAAA	AAAAAAAAAA

FIG. 1D(2)

LTLWSPCLLS	SPAASF*HSL	HLPF*FRSKE	ADMSSAPSPG	TGSPPSPPSN	STTTTPPPAS
APPPTPSSP	PPPSTIPTSP	PPSSRSTPSA	PPSPPTPST	PGSPPPLPQP	SPPAPTPGS
PPAPVTPPTR	NPPPSVPGPP	SNPSREGGSP	RPPSSPSPPS	PSSDGLSTGV	VVGIAIGGVA
LLVIVTLICL	LCKKKRRRDE	EDAYVPPP	PPGPKAGGPY	GGQQQQWRQQ	NATPPSDHVV
TSLPPPCKAP	SPPRQPPPPP	PPPFMSSSGG	SDYSDRPVLP	PPSPGLVLF	SKSTFTYEEL
ARATNGFSEA	NLLGQGGFGY	VHKGVLPNGK	EVAVKQLKVG	SGQGEREFQA	EVEIISRVHH
RHLVSLVGYC	IAGAKRLLVY	EFVPNNNLEL	HLHGEGRPTM	EWSTRLKIAL	GSAKGLSYLH
EDCNPKIIR	DIKASNILID	FKEAKVADF	GLAKIASDTN	THVSTRVMGT	FGYLAPEYAA
SGKLTEKSDV	FSFGVVLLLEL	ITGRRPV DAN	NVYVDDSLVD	WARPLLN RAS	EQGDFEGLAD
AKMNNNGYDRE	EMARMVACAA	ACVRHSARR	PRMSQIVRAL	EGNVSLSDLN	EGMRPGQSNV
YSSYGGSTDY	DSSQYNEDMK	KFRKMA LGTQ	EYNATGEYSN	PTSDYGLYPS	GSSSEGQTTR
EMEMGKIKRT	GQGYSGPSL	TRWERN*RVF	FHYFFKTVKI	*ENCLTLIKT	TTI*GYNTF*
IGF*KKKKK					

FIG. 1E

FIG. 2B

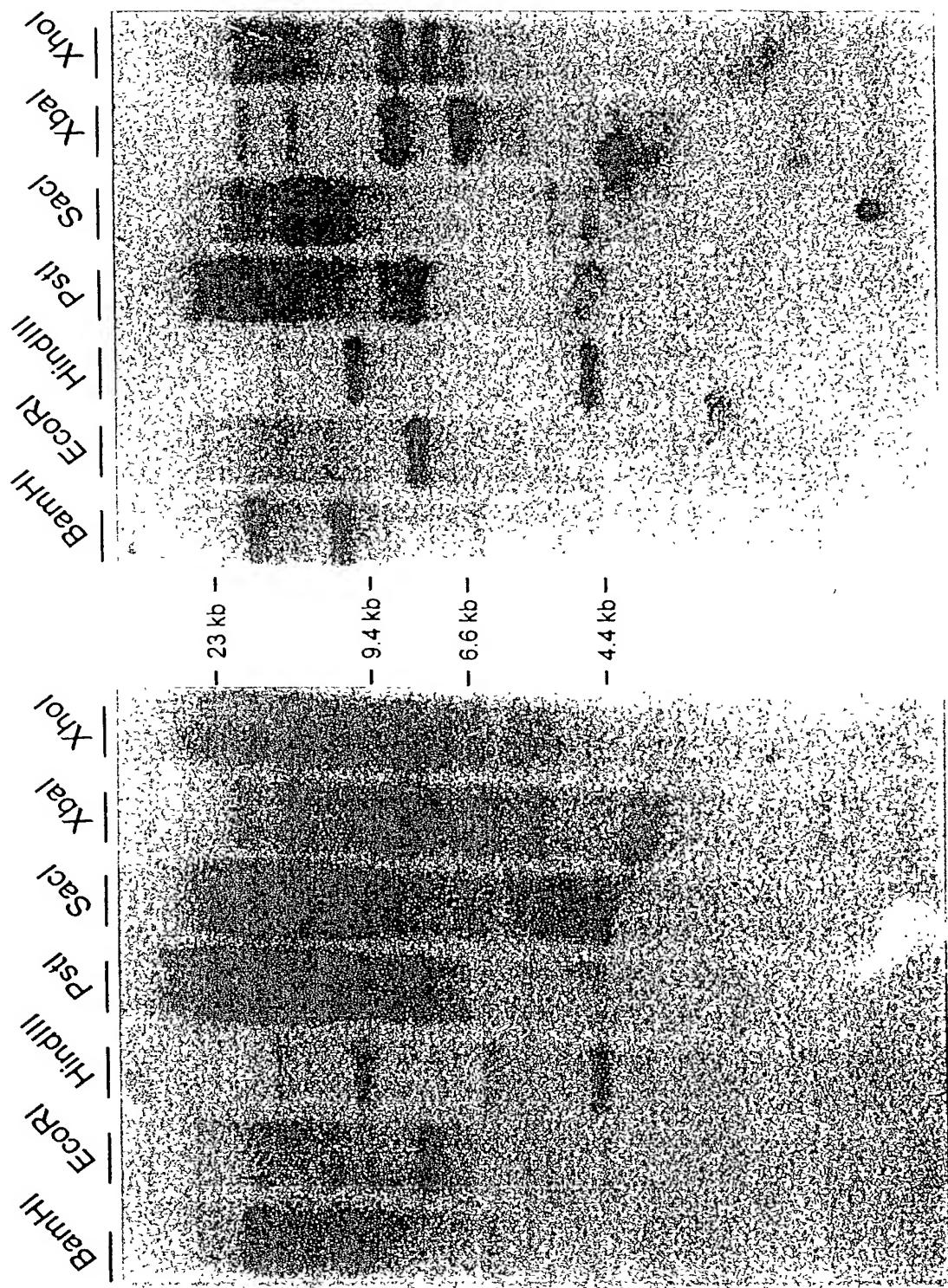


FIG. 2A

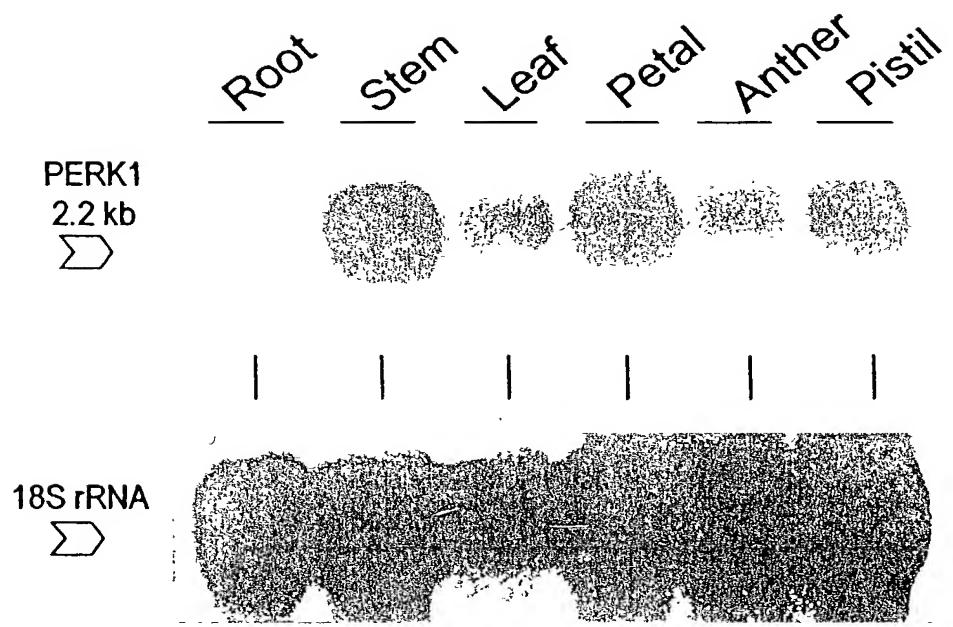


FIG. 3

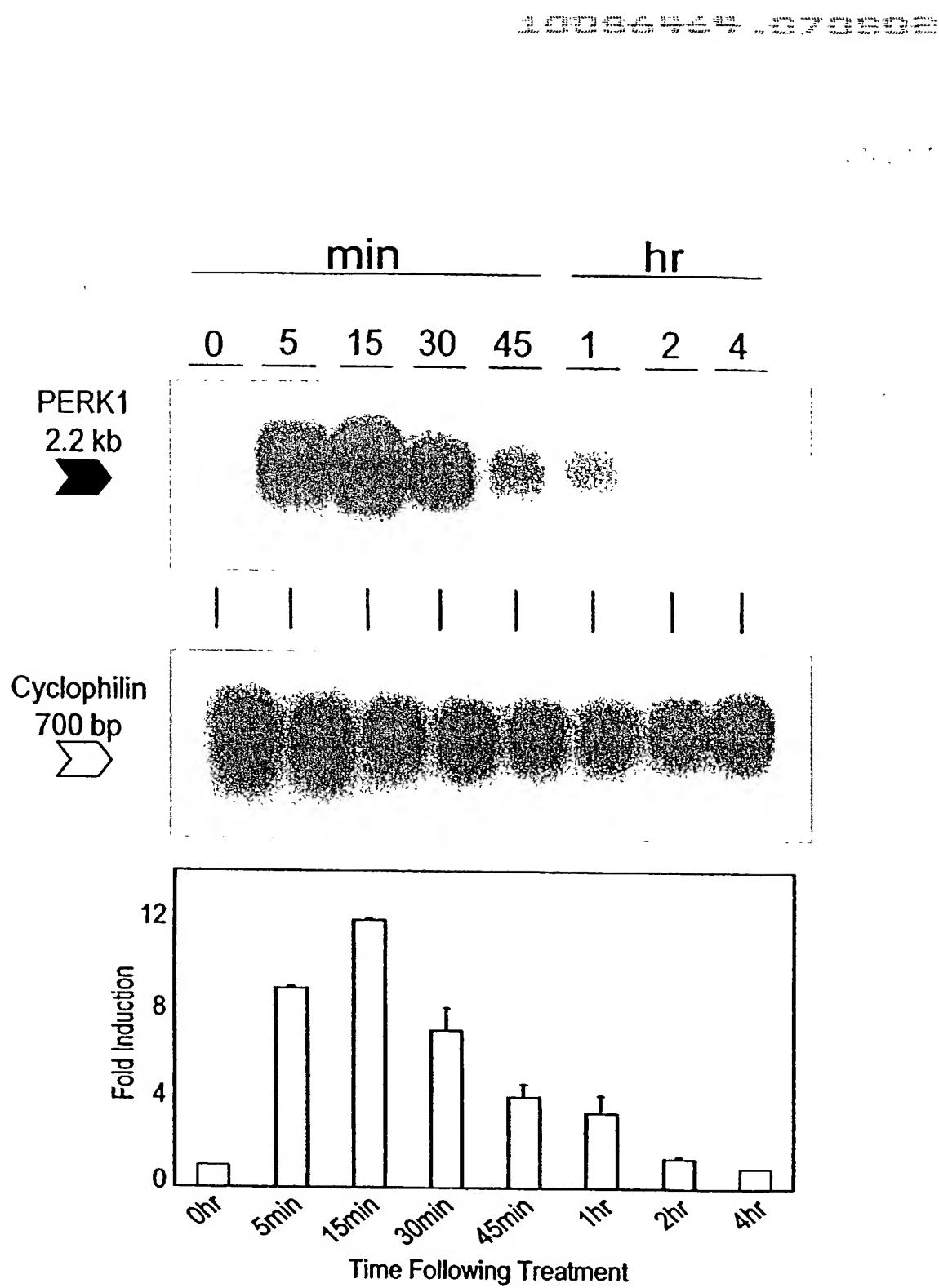


FIG. 4A(1)

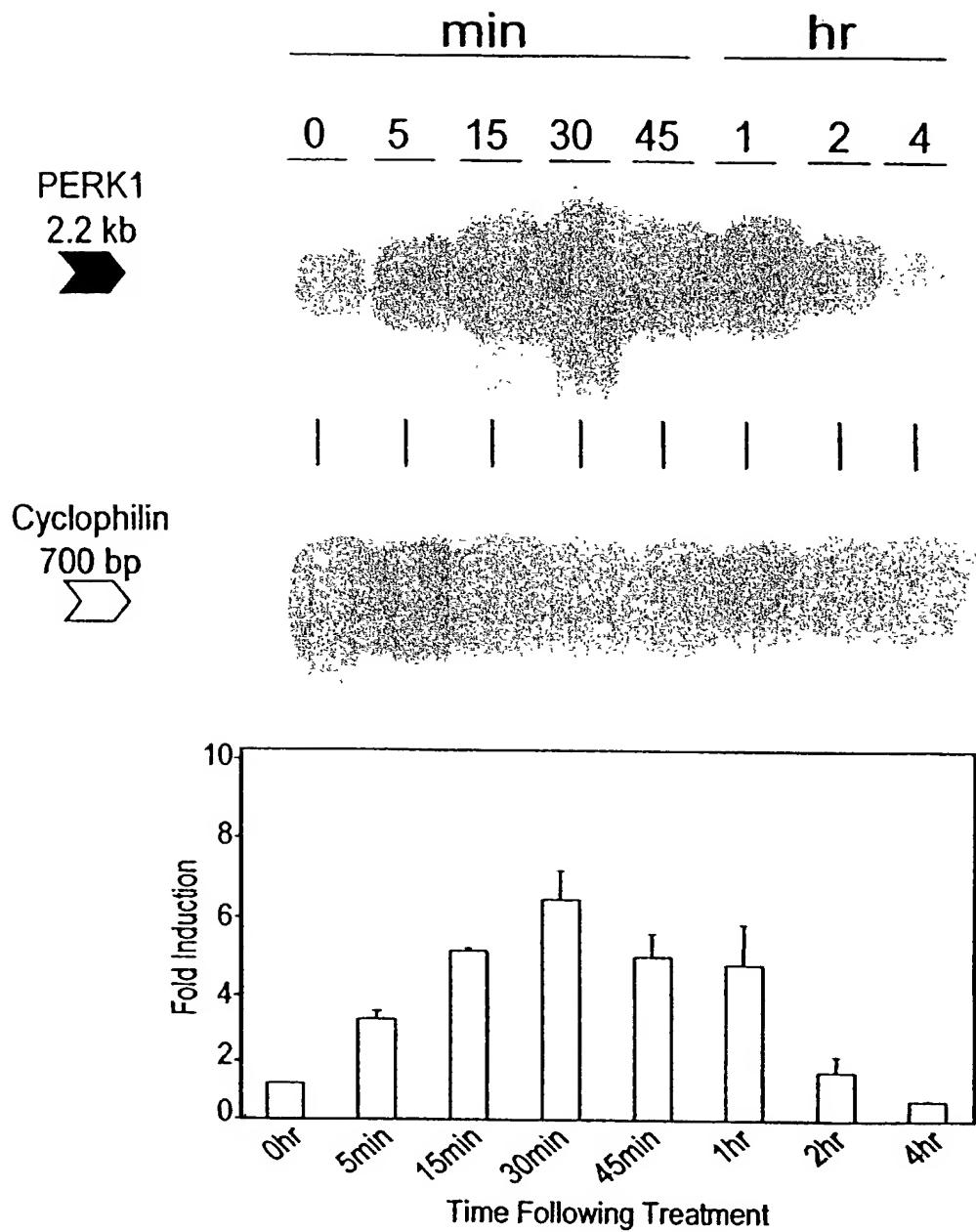


FIG. 4A(2)

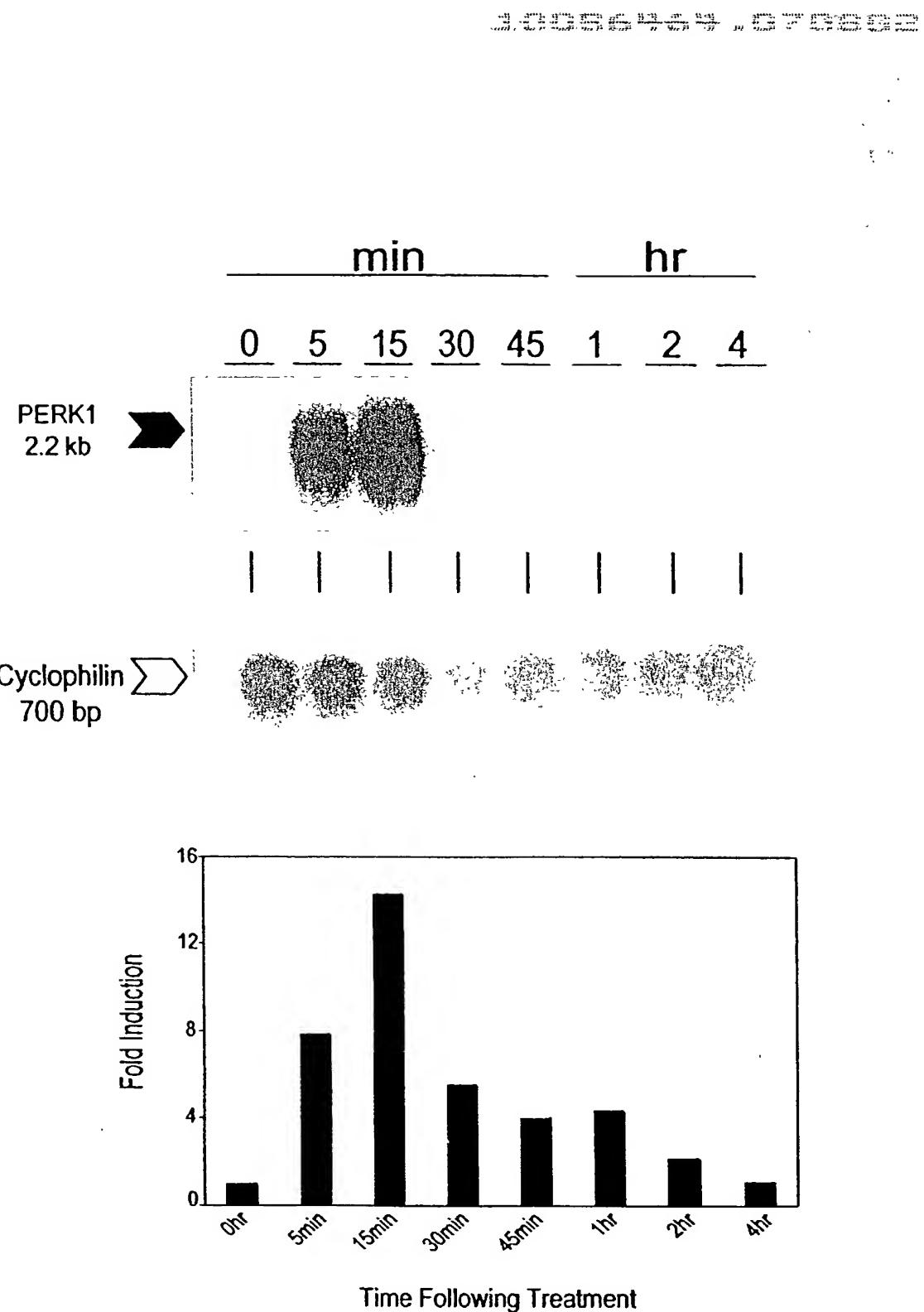


FIG. 4B

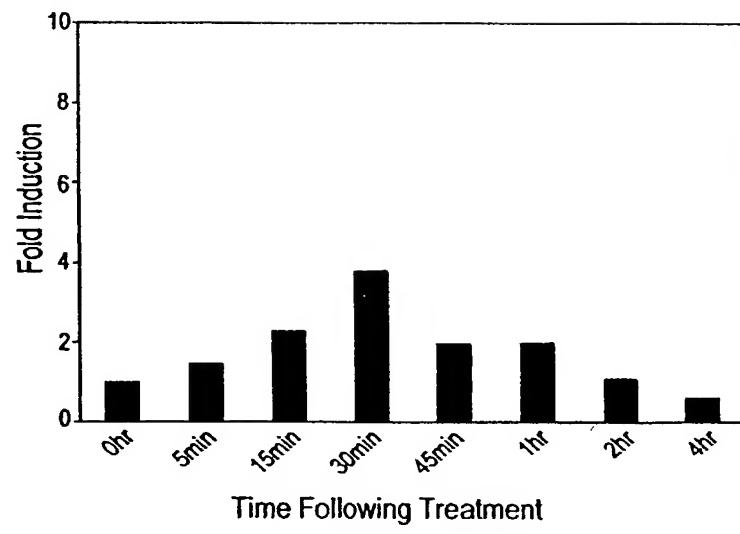
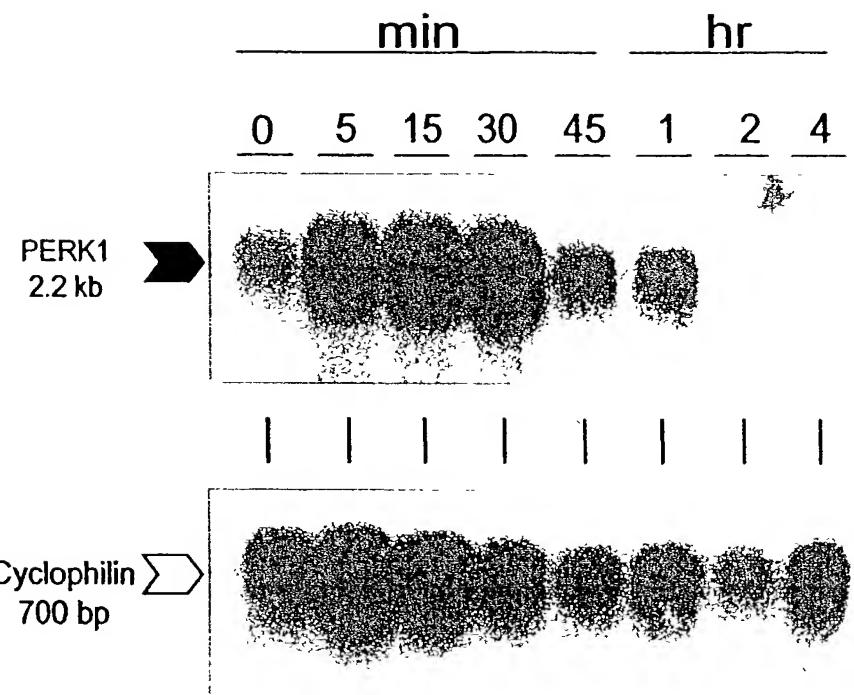


FIG. 4C(1)

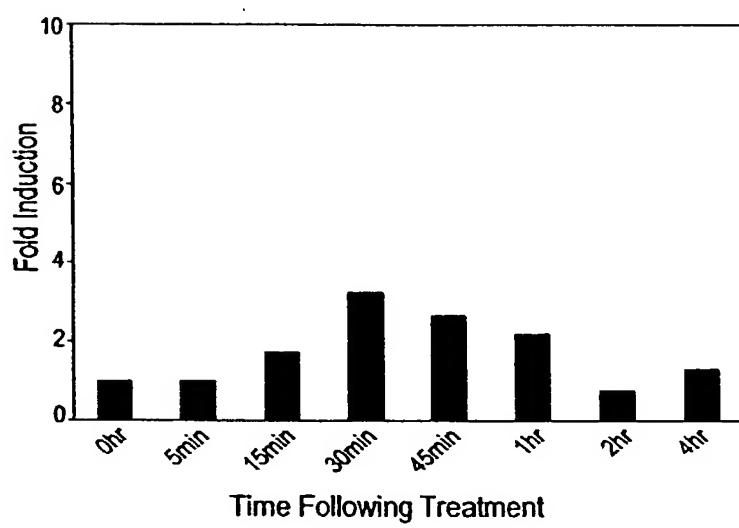
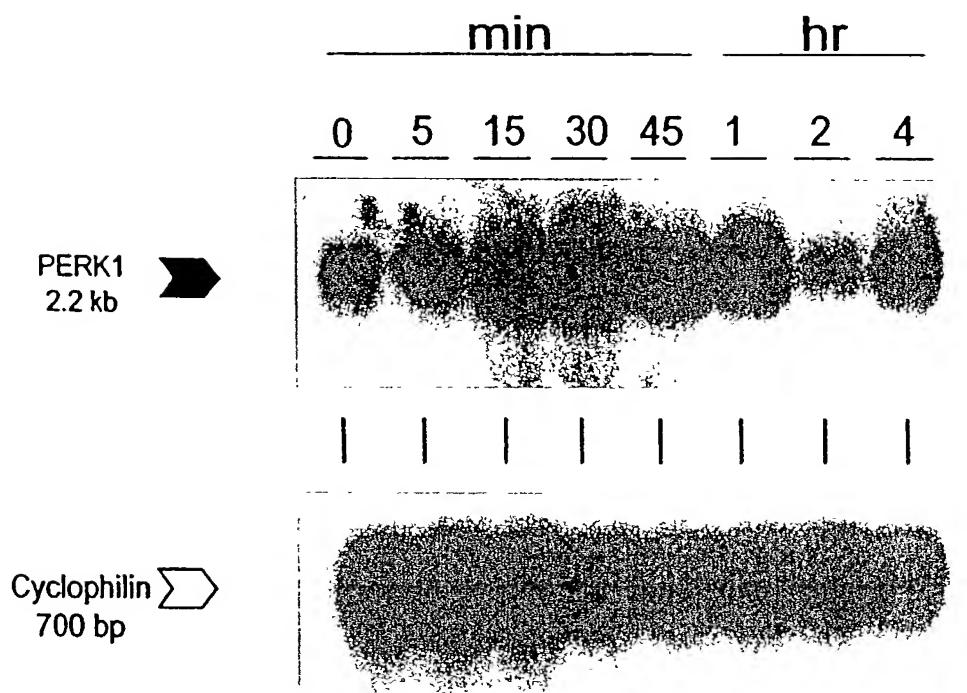


FIG. 4C(2)

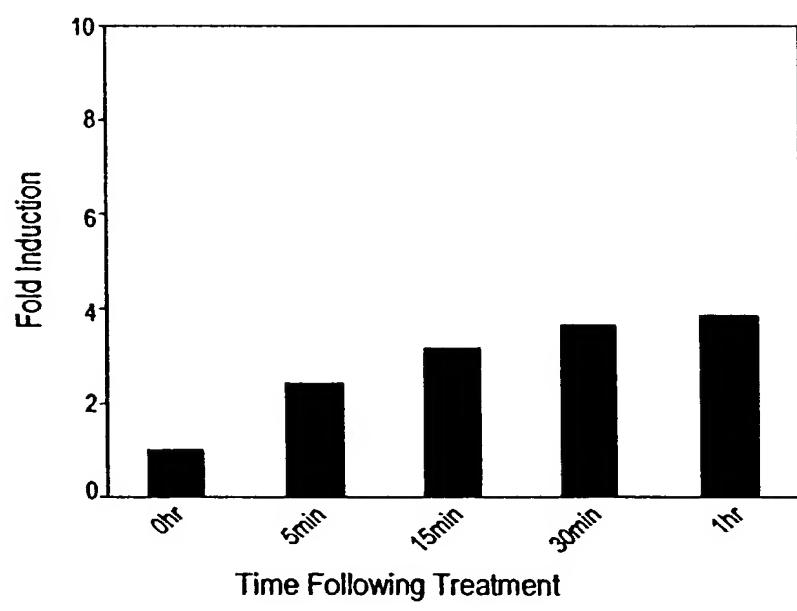
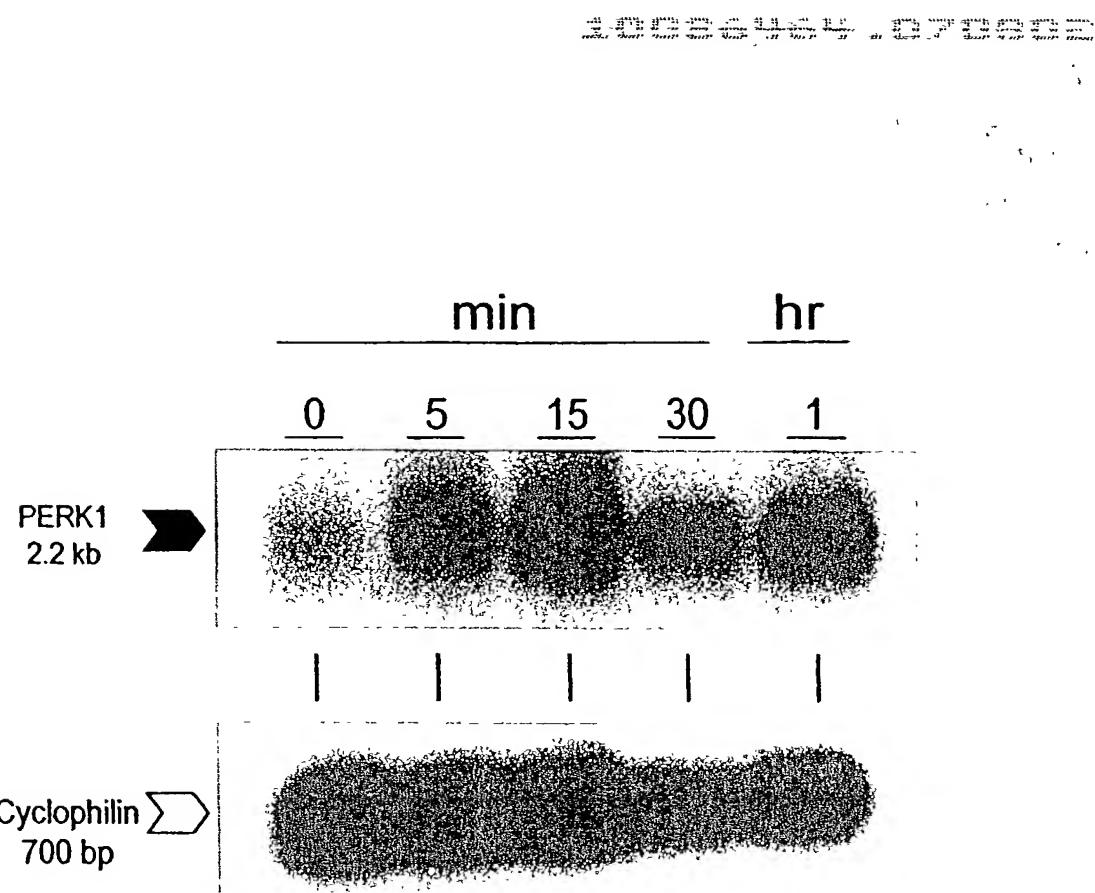


FIG. 4D

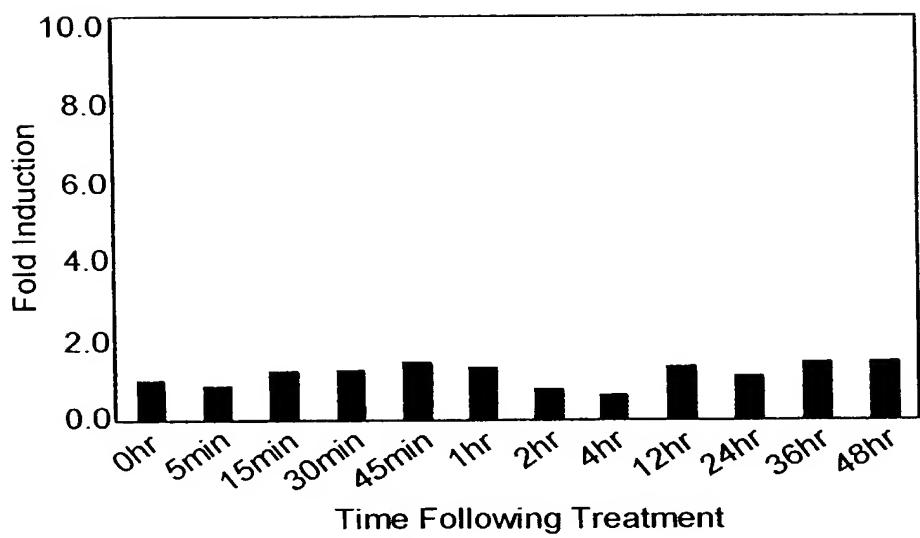
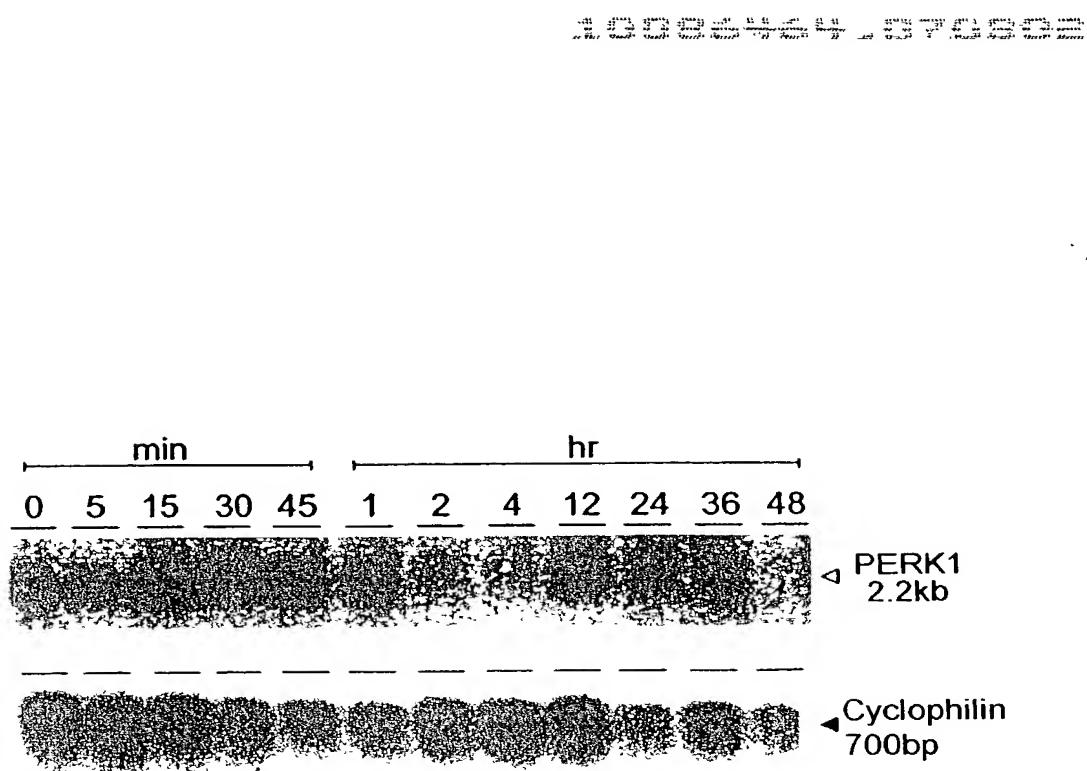


FIG. 5A

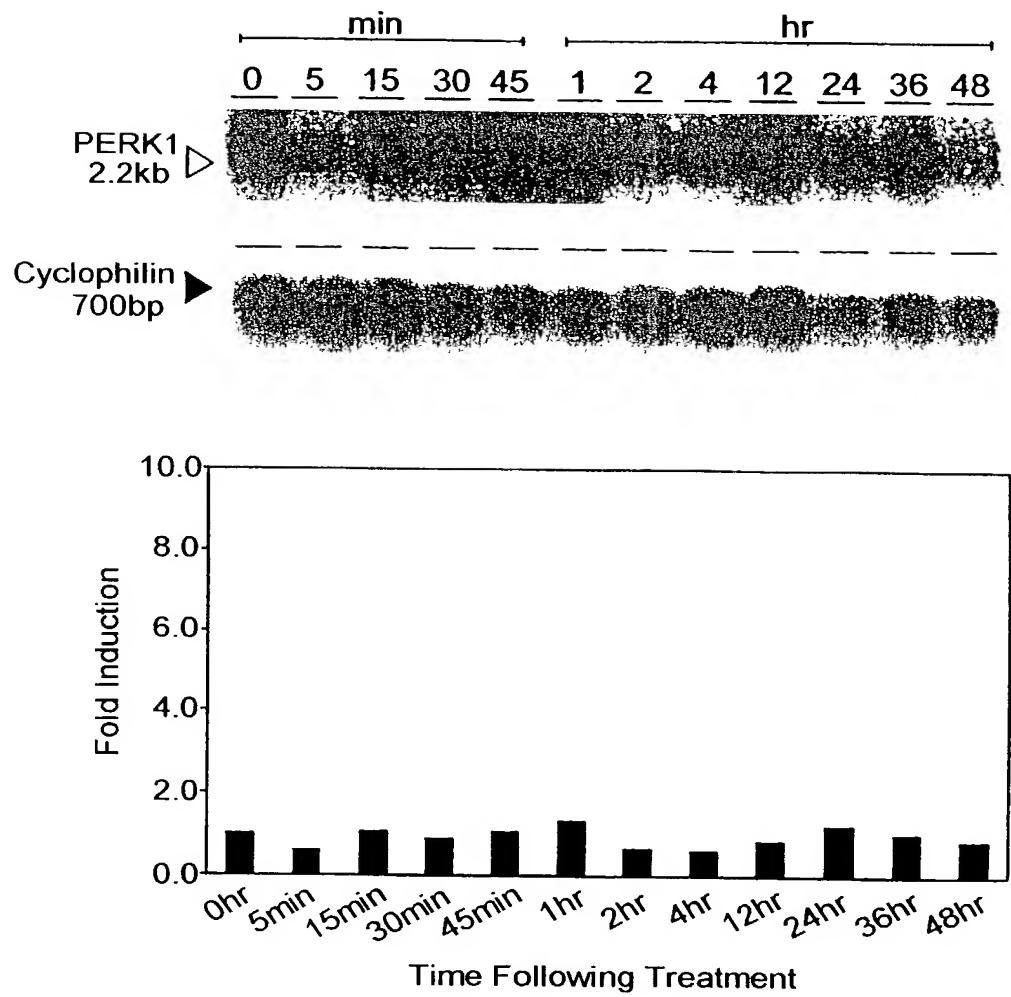


FIG. 5B

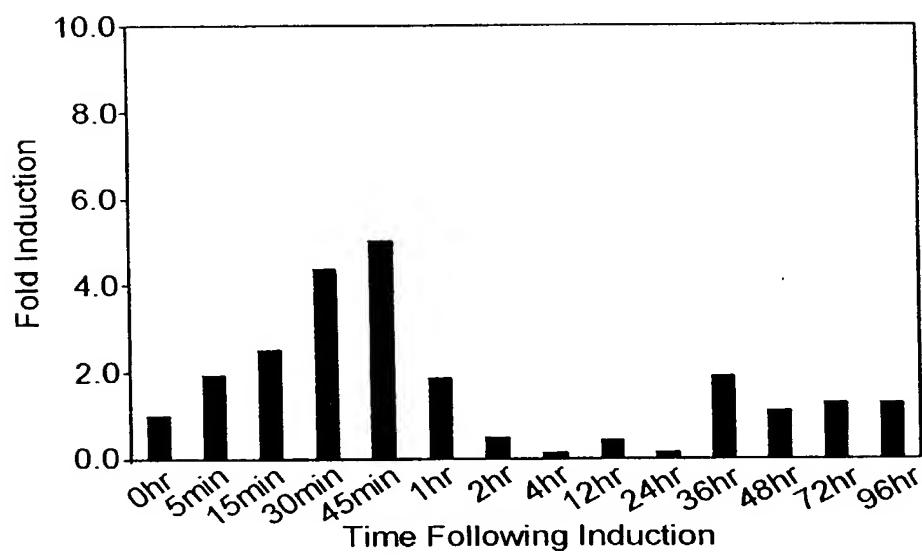
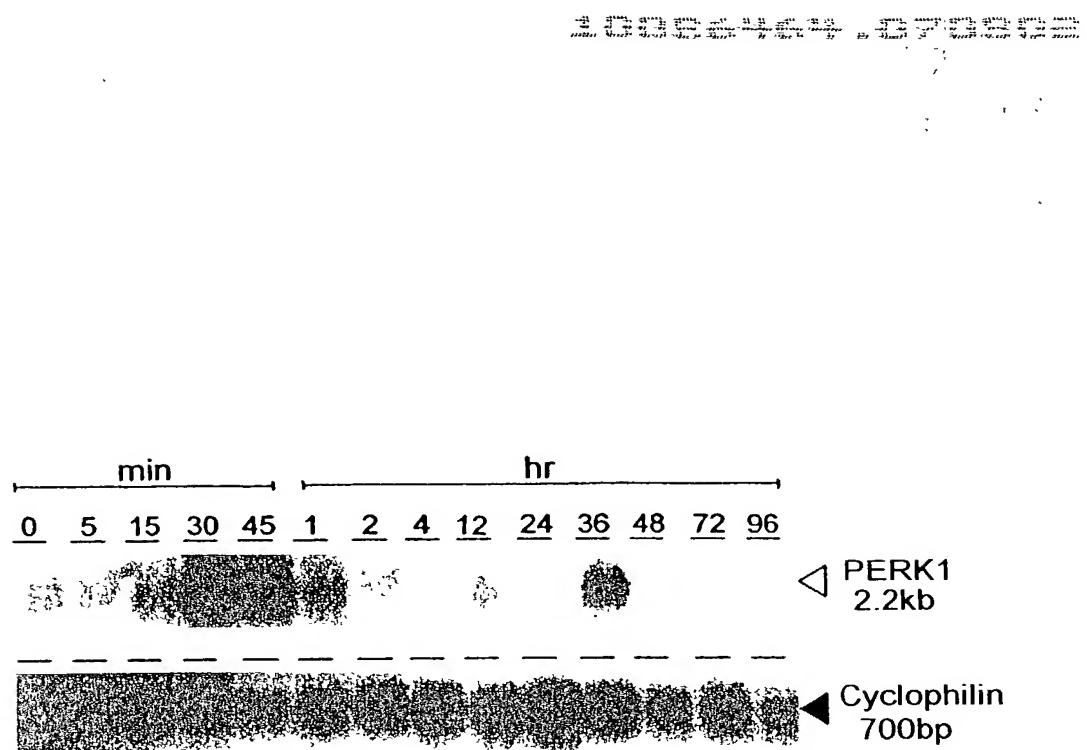


FIG. 6A

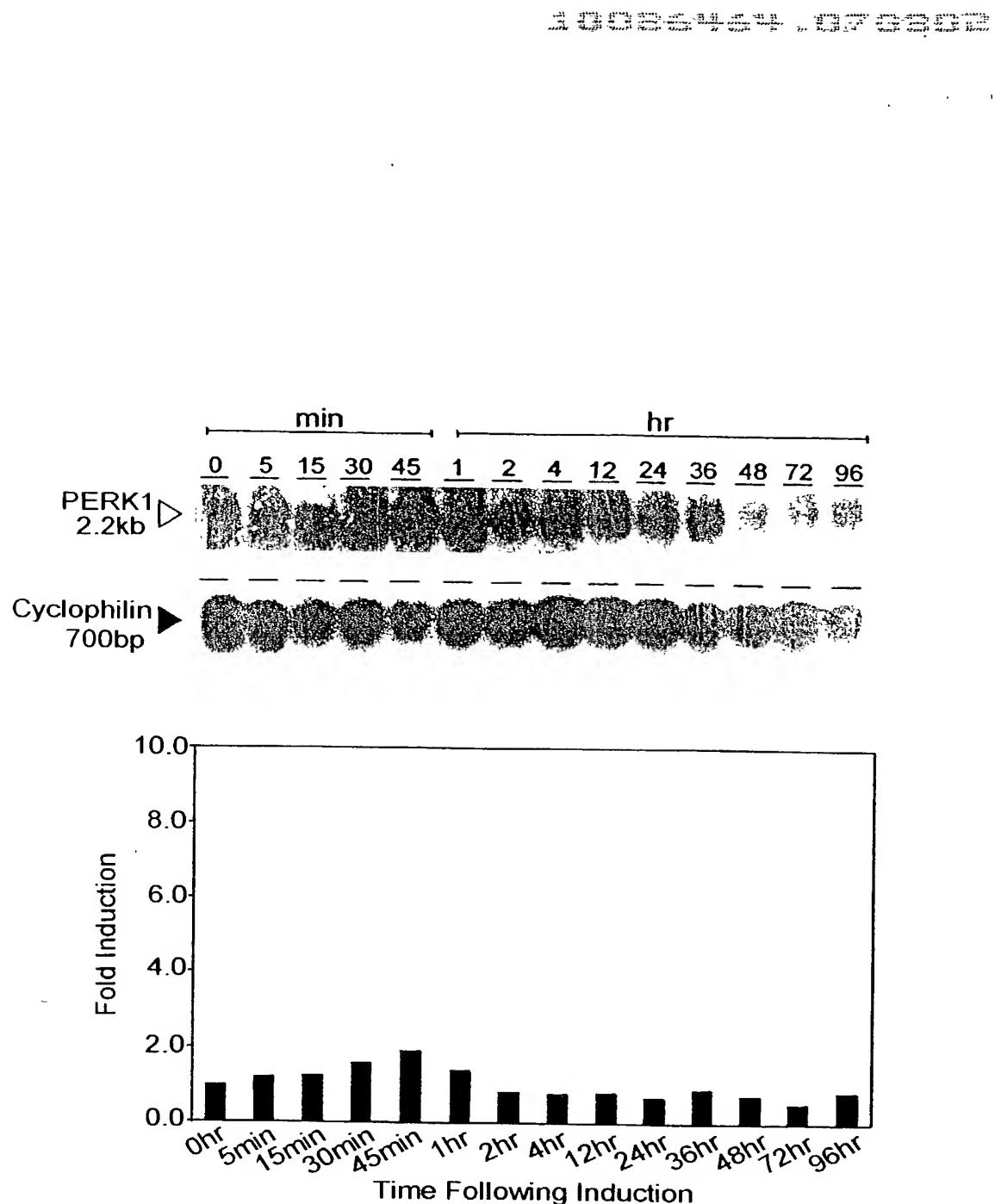


FIG. 6B

• Fungal pathogen : *Sclerotinia sclerotiorum*

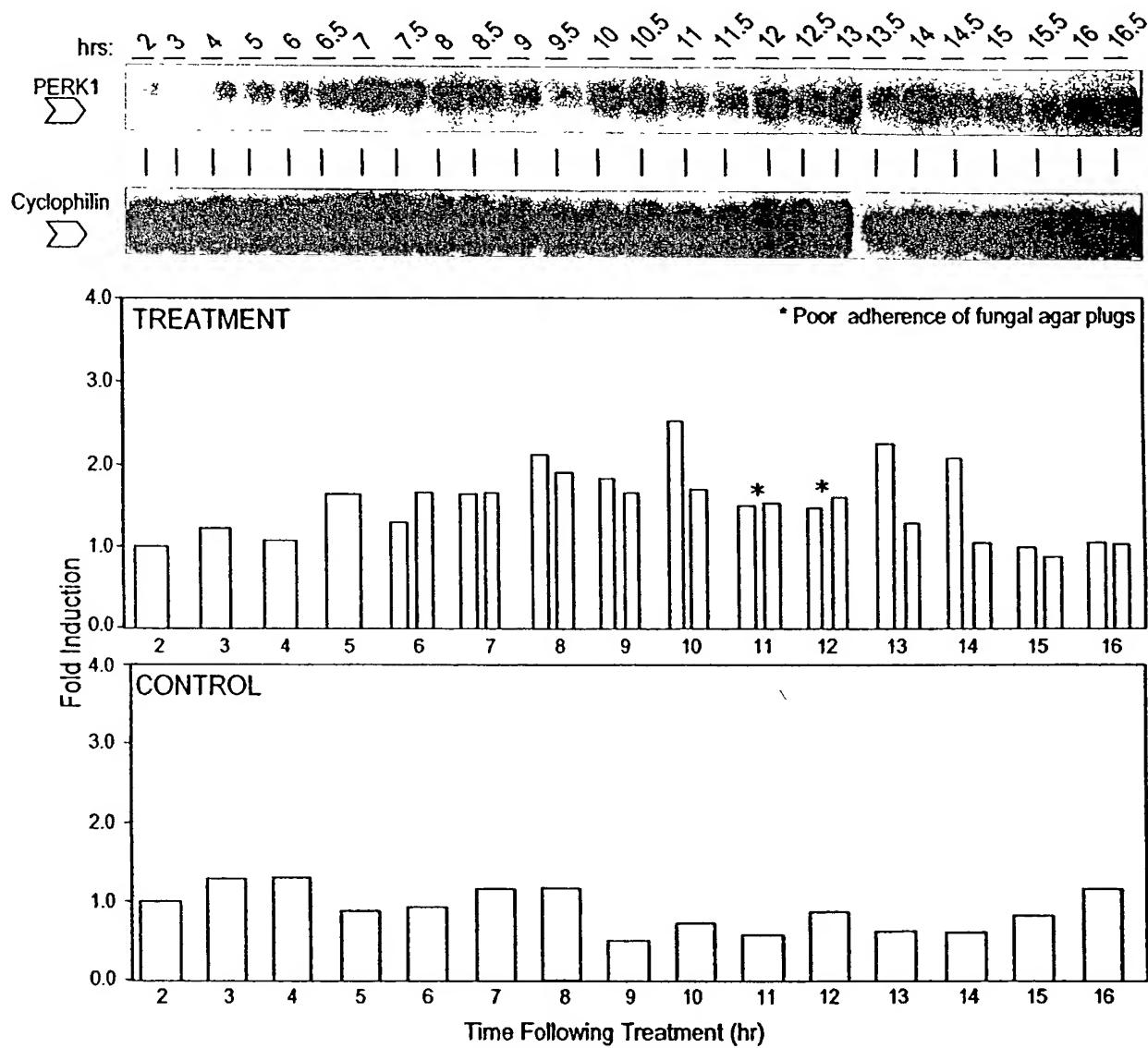


FIG. 7

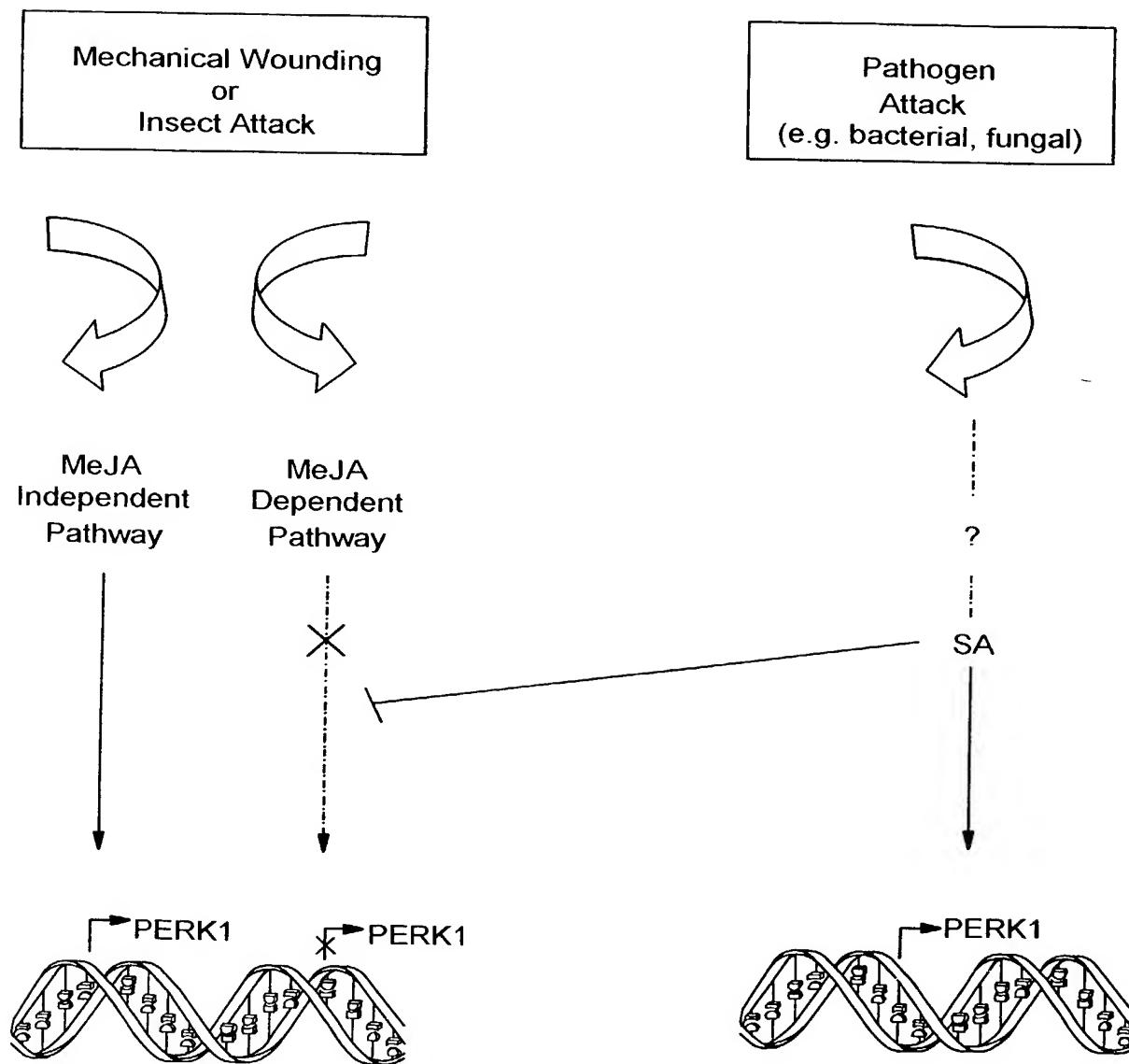


FIG. 8

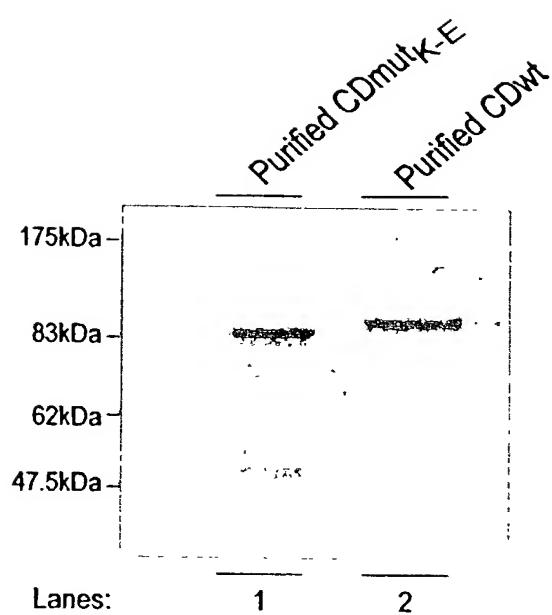


FIG. 9A

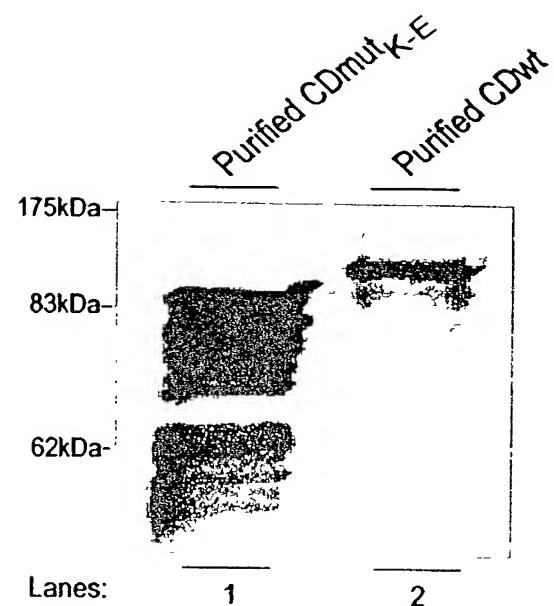


FIG. 9B

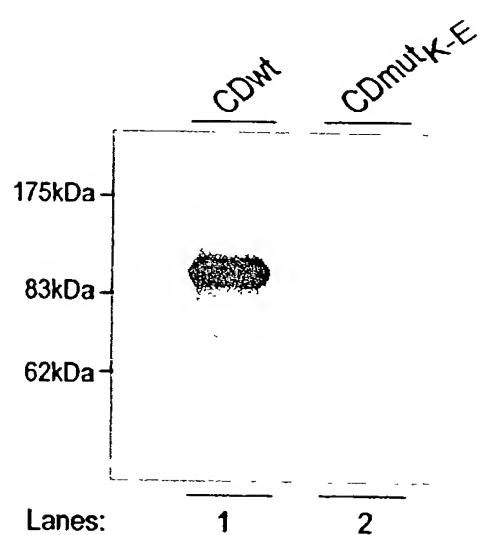


FIG. 9C

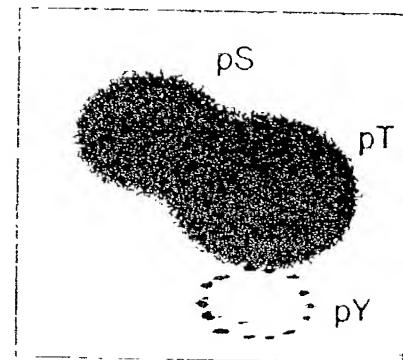


FIG. 9D

	1	138	160	648
PERK1	ELE	TM	KINASE	
	1	247	268	731
†AAC98010	ELE	TM	KINASE	
	36% (76-211)	30%	50% (330-704)	
	1	150	172	633
† AAD15491	ELE	TM	KINASE	
	36% (5-134)	30%	64% (173-614)	
	1	180	194	674
† CAA18823	ELE	TM	KINASE	
	36% (1-133)	33%	52% (214-674)	
	1	280	303	731
† CAA18590	ELE	TM	KINASE	
	32% (50-185)	33%	63% (370-710)	

All have no signal peptide and predicted to be Type1b integral membrane proteins

† Predicted proteins from the Arabidopsis genome sequencing project.

ELE: Extensin-like extracellular ; TM: Transmembrane domain ; Red = sequence identity to PERK1 domain

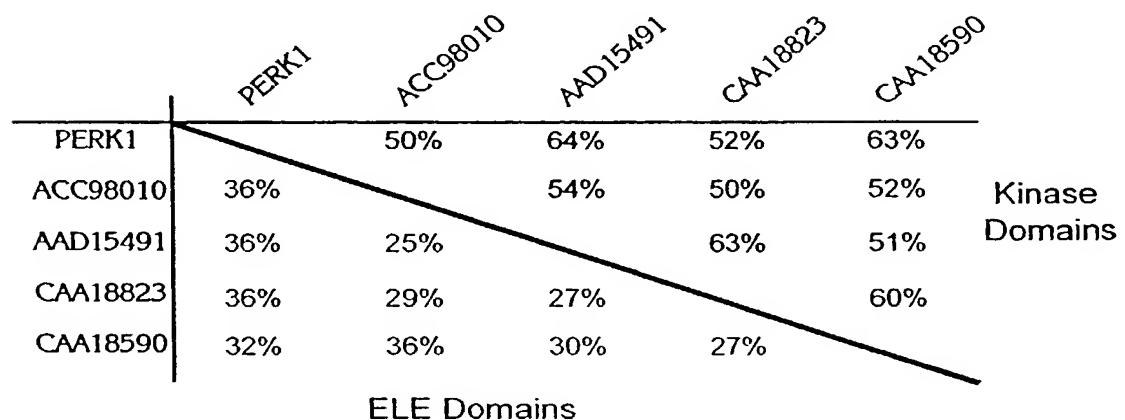


FIG. 10

TAGAAAAAAA AAAATGTCAG ACTTAGGCGA GTCGCCGAGT TCTTCACCAC CAGCACCAC
AGCTGATACC GCTCCCTCAC CAGAGACTCC ATCAGAAAAC TCAGCTCTTC CACCTGTTGA
TTCCCTCTCCT CCTAGTCCAC CAGCTGATTC ATCATCAACA CCGCCGCTGT CAGAACCATC
CACTCCTCCT CCAGATTAC AGCTTCCTCC TTTACCTTCG ATTCTTCCTC CGCTAACAGA
TTCTCCACCT CCACCTTCCG ATTCTTCCTCC ACCCGTTGAT TCAACCCCTT CTCCGCCGCC
ACCGACGTCA AACGAATCTC CTTCTCCTCC AGAAGATTCC GAAACACCAC CTGCTCCACC
AAATGAATCC AATGACAACA ACCCTCCTCC GTCTCAAGAT CTTCAATCGC CTCCCTCCATC
GTCGCCGTCG CCGAATGTAG GACCCACAAA CCCGGAATCA CCACCGTTAC AATCTCCTCC
AGCTCCACCA GCATCAGATC CTACAAATTAC ACCGCCAGCT TCACCATTAG ACCCTACCAA
TCCTCCCCCA ATACAACCAC CAGGACCAGC CACTTCTCCT CC GGCTAATC CCAACGCTCC
GCCGAGCCCA TTCCCCACAG TACCACCCAA AACTCCTTCT AGTGGACCTG TGGTGTCTCC
ATCTCTCACA TCCCCTAGTA AAGGAACCTCC TACTCCAAAC CAAGGCAATG GAGATGGCGG
TGGCGGTGGT GGCGCTATC AAGGGAAGAC TATGGTTGGT ATGGCTGTAG CCGGTTTCGC
AATCATGGCG CTTATAGGCG TTGTGTTCTT AGTGAGAAGA AAGAAAAAGA GAAACATTGA
TAGCTATAAT CACTCACAGT ACTTGCCACA TCCAATTTC TCTGTTAAAT CAGGTTAAA
AATCTCACCT TTATCTCTCT CTGATCATCT TCTATGTGCT TGAATCATCT CTCTGACTAT
CTTGCTTTT GATGTAGATG GATTCTTATA CGGTCAAGAT CCAGGTAAAG GATACTCCTC
TGGTCCTAAT GGTTCAATGT ATAACAATTAC ACAGCAACAA CAATCCTCTA TGGGAAACAG
TTATGGTACA GCTGGTGGTG GTTATCCTCA TCATCAAATG CAATCAAGTG GCACACCTGA
CTCTGCTATA CTCGGAAGTG GCCAGACTCA TTTCAGTTAC GAAGAGCTTG CTGAGATAAC
ACAAGGCTTT GCTCGAAAAA ACATTCTGG AGAAGGCGGA TTTGGATGTG TCTATAAAGG
TACATTGCAG GATGGTAAAG TTGTTGCCGT TAAGCAGCTT AAAGCTGGAA GTGGACAAGG
TGACCGTGAA TTCAAAGCAG AGGTTGAGAT CATCAGCCGC GTTCATCATC GCCATTGGT
CTCTCTGGTT GGTTACTGCA TTTCAGACCA GCATAGATTG CTTATCTATG AGTATGTTTC

FIG. 11A(1)

TAATCAAACC TTGGAGCATC ATTTGCATGG TGAGTGACTT GTTACCATTT TCGTTATAGA
TAAGACTTTT TTTTAGCTTT ACGTGTAGA CTGACTCGCT TTACGCTTTA GGAAAGGGTT
TGCCAGTTTT AGAGTGGTCT AAGAGAGTCC GGATCGCTAT AGGATCAGCC AAAGGGTTGG
CATATCTTCA CGAAGACTGT AAGTAATGCC TTCACATTT CTTAGTTGTG TGCTTTGGTT
ATGCACTTCA TAGTTAAC AGAAGCCAAA AATCATATCC TTGTTTATT TTACAGGTCA
TCCGAAAATC ATTACACAGAG ATATAAAGTC AGCAAATATT CTTCTAGATG ATGAATATGA
AGCTCAGGCCA ATAATGAAAT CCTCCTTTTC GTTAAATCTA TCTTATGACT GTAAAGTTT
AGTTAATGAG ACTTGTTCTG TTTTTGGAT GTTAGGTTG CTGATTTGG ACTTGCTAGA
CTCAATGATA CAACACAAAC TCATGTTCA ACTCGGGTTA TGGGAACCTT CGGGTAAGCA
AACATTACATC ACAAACTCTA CTCCAAAACT GGACCTTATT GATCCAATGC CTGATGAAA
GTTTGTATA TATGGCTTGA GGCAACAAAT TGGATCAAAC CTGAATCTTT ATTGATCGTA
TGGCTGCATG ACATGTTTG TGTAAAGGTA CCTAGCGCCG GAATATGCAT CAAGTGGAAA
ATTGACTGAT AGATCCGATG TATTCTCATT CGGGTTGTT CTCTTAGAGC TTGTAACTGG
ACGGAAACCA GTTGACCAGA CTCAGCCTCT AGGAGAAGAG AGTTGGTTG AATGGTAAG
AATCCAACCTT TCAAACATTC TTCAATAATA GTAAGATTGG CCCTAGTATA CTTATATAGT
ACTTATAAAAT GAACTCACAG GCGCGCCCGC TGCTTCTCAA AGCCATTGAG ACCGGAGATT
TAAGCGAACT GATTGATACA CGGCTGAAA AGCGTTATGT GGAGCATGAA GTCTTCAGAA
TGATCGAGAC AGCCGCTGCA TGTGTTAGAC ATTCTGGTCC AAAACGCCCA CGCATGGTTC
AGGTAATTCT GACTAACCAA AAGTCCAAAG CTCCCATATA TAGTAACAAG TGATTCTCA
CATCTGAAAA CTTATCTACT CTTCGAAATA AGGTTGTGAG AGCATTGGAC TGCGACGGAG
ACTCGGGAGA TATTAGCAAC GGAATCAAAA TTGGGCAAAG CACAACCTTAT GACTCAGGGC
AATACAATGA AGACATTATG AAATTCAGGA AAATGGCGTT TGGTGGTGT AACAGCGTAG
AGTCAGGATT GTACAGTGGA AACTACTCTG CCAAAAGCTC TTCAGATTTC TCAGGGAATG
AATCTGAGAC TCGGCCTTTC AACAAACCGAC GGTTCTGATC ATACAATAGG TGAAAGTAAC

FIG. 11A(2)

1	M	S	D	L	G	E	S	P	S	S	S	P	P	A	P	P	A	D	T	A	20
1	ATG	TCA	GAC	TTA	GGC	GAG	TCG	CCG	AGT	TCT	TCA	CCA	CCA	GCA	CCA	GCT	GAT	ACC	GCT		60
21	P	P	P	E	T	P	S	E	N	S	A	L	P	P	V	D	S	S	P	P	40
61	CCT	CCA	CCA	GAG	ACT	CCA	TCA	GAA	AAC	TCA	GCT	CTT	CCA	CCT	GTT	GAT	TCC	TCT	CCT	CCT	120
41	S	P	P	A	D	S	S	S	T	P	P	L	S	E	P	S	T	P	P	P	60
121	AGT	CCA	CCA	GCT	GAT	TCA	TCA	TCA	ACA	CCG	CCG	CTG	TCA	GAA	CCA	TCC	ACT	CCT	CCT	CCA	180
61	D	S	Q	L	P	P	L	P	S	I	L	P	P	L	T	D	S	P	P	P	80
181	GAT	TCA	CAG	CTT	CCT	CCT	TTA	CCT	TCG	ATT	CTT	CCT	CCG	CTA	ACA	GAT	TCT	CCA	CCT	CCA	240
81	P	S	D	S	S	P	P	V	D	S	T	P	S	P	P	P	T	S	N	100	
241	CCT	TCC	GAT	TCT	TCT	CCA	CCC	GTT	GAT	TCA	ACC	CCT	TCT	CCG	CCG	CCA	CCG	ACG	TCA	AAC	300
101	E	S	P	S	P	P	E	D	S	E	T	P	P	A	P	P	N	E	S	N	120
301	GAA	TCT	CCT	TCT	CCT	CCA	GAA	GAT	TCC	GAA	ACA	CCA	CCT	GCT	CCA	CCA	AAT	GAA	TCC	AAT	360
121	D	N	N	P	P	P	S	Q	D	L	Q	S	P	P	P	S	S	P	S	P	140
361	GAC	AAC	AAC	CCT	CCT	CCG	TCT	CAA	GAT	CTT	CAA	TCG	CCT	CCA	TCG	TCG	CCG	TCG	CCG	CCG	420
141	N	V	G	P	T	N	P	E	S	P	P	L	Q	S	P	A	P	P	A	P	160
421	AAT	GTA	GGA	CCC	ACA	AAC	CCG	GAA	TCA	CCA	CCG	TTA	CAA	TCT	CCT	CCA	GCT	CCA	CCA	GCA	480
161	S	D	P	T	N	S	P	P	A	S	P	L	D	P	T	N	P	P	P	I	180
481	TCA	GAT	CCT	ACA	AAT	TCA	CCG	CCA	GCT	TCA	CCA	TTA	GAC	CCT	ACC	AAT	CCT	CCC	CCA	ATA	540
181	Q	P	S	G	P	A	T	S	P	P	A	N	P	N	A	P	P	S	P	F	200
541	CAA	CCA	TCA	GGA	CCA	GCC	ACT	TCT	CCT	CCG	GCT	AAT	CCC	AAC	GCT	CCG	CCG	AGC	CCA	TTC	600
201	P	T	V	P	P	K	T	P	S	S	G	P	V	V	S	P	S	L	T	S	220
601	CCC	ACA	GTA	CCA	CCC	AAA	ACT	CCT	TCT	AGT	GGA	CCT	GTG	GTG	TCT	CCA	TCT	CTC	ACA	TCC	660
221	P	S	K	G	T	P	T	P	N	Q	G	N	G	D	G	G	G	G	G	240	
661	CCT	AGT	AAA	GGA	ACT	CCT	ACT	CCA	AAC	CAA	GGC	AAT	GGA	GAT	GGC	GGT	GGC	GGT	GGT	GGC	720
241	G	Y	Q	G	K	T	M	V	G	M	A	V	A	G	F	A	I	M	A	L	260
721	GGC	TAT	CAA	GGG	AAG	ACT	ATG	GTT	GGT	ATG	GCT	GTA	GCC	GGT	TTC	GCA	ATC	ATG	GCG	CTT	780
261	I	G	V	V	F	L	V	R	R	K	K	K	R	N	I	D	S	Y	N	H	280
781	ATA	GCC	GTT	GTG	TTC	TTA	GTG	AGA	AGA	AAG	AAA	AAG	AGA	AAC	ATT	GAT	AGC	TAT	AAT	CAC	840
281	S	Q	Y	L	P	H	P	N	F	S	V	K	S	D	G	F	L	Y	G	Q	300
841	TCA	CAG	TAC	TTG	CCA	CAT	CCC	AAT	TTC	TCT	GTT	AAA	TCA	GAT	GGA	TTC	TTA	TAC	GGT	CAA	900
301	D	P	G	K	G	Y	S	S	G	P	N	G	S	M	Y	N	N	S	Q	Q	320
901	GAT	CCA	GGT	AAA	GGA	TAC	TCC	TCT	GGT	CCT	AAT	GGT	TCA	ATG	TAT	AAC	AAT	TCA	CAG	CAA	960
321	Q	Q	S	S	M	G	N	S	Y	G	T	A	G	G	G	Y	P	H	H	Q	340
961	CAA	CAA	TCC	TCT	ATG	GGA	AAC	AGT	TAT	GGT	ACA	GCT	GGT	GGT	GGT	TAT	CCT	CAT	CAT	CAA	1020
341	M	Q	S	S	G	T	P	D	S	A	I	L	G	S	G	Q	T	H	F	S	360
1021	ATG	CAA	TCA	AGT	GGC	ACA	CCT	GAC	TCT	GCT	ATA	CTC	GGA	AGT	GGC	CAG	ACT	CAT	TTC	AGT	1080
361	Y	E	E	L	A	E	I	T	Q	G	F	A	R	K	N	I	L	G	E	G	380
1081	TAC	GAA	GAG	CTT	GCT	GAG	ATA	ACA	CAA	GGC	TTT	GCT	CGC	AAA	AAC	ATT	CTT	GGA	GAA	GGC	1140
381	G	F	G	C	V	Y	K	G	T	L	Q	D	G	K	V	V	A	V	K	Q	400
1141	GGA	TTT	GGA	TGT	GTC	TAT	AAA	GGT	ACA	TTG	CAG	GAT	GGT	AAA	GTT	GTT	GCG	GTT	AAG	CAG	1200
401	L	K	A	G	S	G	Q	G	D	R	E	F	K	A	E	V	E	I	I	S	420
1201	CTT	AAA	GCT	GGA	AGT	GGA	CAA	GGT	GAC	CGT	GAA	TTC	AAA	GCA	GAG	GTT	GAG	ATC	ATC	AGC	1260
421	R	V	H	H	R	H	L	V	S	L	V	G	Y	C	I	S	D	Q	H	R	440
1261	CGC	GTT	CAT	CAT	CGC	CAT	TTG	GTC	TCT	CTG	GTT	GGT	TAC	TGC	ATT	TCA	GAC	CAG	CAT	AGA	1320
441	L	L	I	Y	E	Y	V	S	N	Q	T	L	E	H	H	L	H	E	W	S	460
1321	TTC	CTT	ATC	TAT	GAG	TAT	GTT	TCT	AAT	CAA	ACC	TTG	GAG	CAT	CAT	TTG	CAT	GAG	TGG	TCT	1380
461	K	R	V	R	I	A	I	G	S	A	K	G	L	A	Y	L	H	E	D	C	480
1381	AAG	AGA	GTC	CGG	ATC	GCT	ATA	GGA	TCA	GCC	AAA	GGG	TTG	GCA	TAT	CTT	CAC	GAA	GAC	TGT	1440
481	H	P	K	I	I	H	R	D	I	K	S	A	N	I	L	L	D	D	E	Y	500
1441	CAT	CCG	AAA	ATC	ATT	CAC	AGA	GAT	ATA	AAG	TCA	GCA	AAT	ATT	CTT	CTA	GAT	GAT	GAA	TAG	1500
501	E	A	Q	A	I	M	K	S	S	F	S	L	N	L	S	Y	D	C	K	V	520
1501	GAA	GCT	CAG	GCA	ATA	ATG	AAA	TCC	TCC	TTT	TCG	TTA	AAT	CTA	TCT	TAT	GAC	TGT	AAA	GTT	1560
521	L	V	A	D	F	G	L	A	R	L	N	D	T	T	Q	T	H	V	S	T	540
1561	TTA	GTT	GCT	GAT	TTT	GGG	CTT	GCT	AGA	CTC	AAT	GAT	ACA	CAA	ACT	CAT	GTT	TCA	ACT		1620

FIG. 11B(1)

541	R	V	M	G	T	F	G	Y	L	A	P	E	Y	A	S	S	G	K	L	T	560
1621	CGG	GTT	ATG	GGA	ACC	TTC	GGG	TAC	CTA	GCG	CCG	GAA	TAT	GCA	TCA	AGT	GGA	AAA	TTG	ACT	1680
561	D	R	S	D	V	F	S	F	G	V	V	L	L	E	L	V	T	G	R	K	580
1681	GAT	AGA	TCC	GAT	GTA	TTC	TCA	TTC	GGG	GTT	GTT	CTC	TTA	GAG	CTT	GTA	ACT	GGA	CGG	AAA	1740
581	P	V	D	Q	T	Q	P	L	G	E	E	S	L	V	E	W	A	R	P	L	600
1741	CCA	GTT	GAC	CAG	ACT	CAG	CCT	CTA	GGA	GAA	GAG	AGT	TTG	GTT	GAA	TGG	GCG	CGC	CCG	CTG	1800
601	L	L	K	A	I	E	T	G	D	L	S	E	L	I	D	T	R	L	E	K	620
1801	CTT	CTC	AAA	GCC	ATT	GAG	ACC	GGA	GAT	TTA	AGC	GAA	CTG	ATT	GAT	ACA	CGG	CTT	GAA	AAG	1860
621	R	Y	V	E	H	E	V	F	R	M	I	E	T	A	A	A	C	V	R	H	640
1861	CGT	TAT	GTG	GAG	CAT	GAA	GTC	TTC	AGA	ATG	ATC	GAG	ACA	GCC	GCT	GCA	TGT	GTT	AGA	CAT	1920
641	S	G	P	K	R	P	R	M	V	Q	V	V	R	A	L	D	C	D	G	D	660
1921	TCT	GGT	CCA	AAA	CGC	CCA	CGC	ATG	GTT	CAG	GTT	GTG	AGA	GCA	TTG	GAC	TGC	GAC	GGA	GAC	1980
661	S	G	D	I	S	N	G	I	K	I	G	Q	S	T	T	Y	D	S	G	Q	680
1981	TCG	GGA	GAT	ATT	AGC	AAC	GGA	ATC	AAA	ATT	GGG	CAA	AGC	ACA	ACT	TAT	GAC	TCA	GGG	CAA	2040
681	Y	N	E	D	I	M	K	F	R	K	M	A	F	G	G	D	N	S	V	E	700
2041	TAC	AAT	GAA	GAC	ATT	ATG	AAA	TTC	AGG	AAA	ATG	GCG	TTT	GGT	GGT	GAT	AAC	AGC	GTA	GAG	2100
701	S	G	L	Y	S	G	N	Y	S	A	K	S	S	S	D	F	S	G	N	E	720
2101	TCA	GGA	TTG	TAC	AGT	GGA	AAC	TAC	TCT	GCC	AAA	AGC	TCT	TCA	GAT	TTC	TCA	GGG	AAT	GAA	2160
721	S	E	T	R	P	F	N	N	R	R	F	*									732
2161	TCT	GAG	ACT	CGG	CCT	TTC	AAC	AAC	CGA	CGG	TTC	TGA									2196

FIG. 11B(2)

GAAAATTTG ATCTCCGATG GCTTCTTCTC CTGAATCTGC TCCTCCAACA AACTCCACCT
CTTCTCCATC TCCACCGTCT AATACCAATT CAACCACCTC TTCTCCGCCG GCTCCGTCTC
CTCCCTCTCC TACACCTCCT CAAGGAGACT CATCATCATC GCCACCTCCT GATTCCACAT
CTCCACCAGC TCCACAAGCT CCTAACCCCTC CTAATTCCCTC TAATAACTCT CCTTCCCCTC
CGTCACAGGG CGGTGGAGGA GAAAGAGGAA ATGGAGGAAA CAATGGTGGC AATGATACTC
CACCGTCACG CGGCTCTCCT CCTTCTCCTC CTTCTAGGAG TAATGGAGAT AATGGTGGTA
GCAGATCATC GCCACCAGGA GACACTGGAG GCTCTCGCTC AGACAACCCCT CCTTCTAGCG
GAGGAAGCAG TGGAGGAGGT GGAGGTGGAA GAAGTAATAC GAATACAGCG ATCATAGTTG
GTGTATTAGT CGGAGCTGGA CTTTGATGA TCGTTCTTAT TATTGTGTGT GTTAGACGCA
AAAAGAAGAG AAAAGACTCC TTCTACCCCTG AACCCATGAA AGGTAAAAAC ATATACACAC
TCTTATGTTT CAACAAATAA GAAGCTTAGA TTCTTCATA AAATTCAGG AAACCAATAT
CAATACTATG GAAACAACAA CAACAACAAT GCTTCACAGA ATTATCCGAA TTGGCACCTA
AATTACAAG GCCAAAACCA ACAATCTACT GGTGGTTGGG GAGGCCGTGG ACCATCACCG
CCTCCTCCCTC CGGGATGCC TACAAGCGGA GAAGATTCTT CCATGTACTC AGGCCCATCA
CGCCCAAGTTT TACCTCCTCC TTGCGCTGCT CTAGCCCTCG GATTCAACAA GAGCACTTT
ACTTACCAAG AGCTTGCAGC TGCAACAGGA GGGTTACGG ATGCTAACCT TTTGGACAG
GGAGGATTG GGTATGTCCA TAAAGGAGTC TTGCCTAGCG GGAAAGAAGT AGCAGTTAAG
AGTTAAAAG CGGGTAGCGG ACAAGGAGAG AGGGAGTTTC AAGCTGAGGT CGATATCATT
AGCCGTGTGC ATCATCGGTA TCTTGTTCCT TTGGTTGGAT ATTGCATAGC TGATGGACAG
AGGATGTTGG TTTATGAGTT TGTTCTAAC AAAACTTTGG AATATCATCT TCATGGTTAG
ACCACTAAA AACTTGAGT ACTAAGTTA TTTTCTCTAA TCTATATATT CAAGAAAGTT
GTAACCTAA TTTGTTGTTG TAGGGAAAAA TCTTCCGGTA ATGGAGTTCT CCACTAGGTT
GCGTATCGCC TTAGGTGCTG CGAAAGGACT CGCTTACCTT CACGAAGACT GTAAAGTTTA
ACATTCACCA TTCTCATTCTT CTTAACCAAG TTGCATAAAA CAGAGAAAGC TCTGTCTCTG

FIG. 12A(1)

ACTAGTGT TA TCTTTTGGC TGAGAAAATG GTGCAGGCCA TCCTCGGATC ATTCAACCGCG
ACATCAAGTC TGCAAATATT CTCTTGGACT TCAACTTGA TGCTATGGTG ATAAACTAGT
AGCTTGCATT CATCTACGGT TTTTTGTTAA GACTACATTG ATGACATTTT GCATTTGTTT
ATTCAAGGTGG CTGATTTGG ATTAGCTAAG TTAACATCTG ATAACAACAC TCATGTATCT
ACTCGTGTGA TGGGAACCTTT CGGGTAAGCG TTTTACCGTA TGATAAGATT GTTCGTGACA
CTCAAGAAC ATAACCTTG TAGACTAATC TACTTGCTT CTTTCCACAA ACATGTGTAG
ATATCTAGCT CCAGAATATG CTTCAAGCGG TAAATTAACC GAGAAATCCG ATGTTTCTC
TTACGGAGTT ATGTTATTGG AACTTATAAC TGGAAAACGA CCGGTTGATA ATAGCATCAC
CATGGACGAC ACCTTAGTAG ATTGGGTATT CATGCATGTA ACATATGTAT CGTGTATATA
TGTTTTCGCG CTTTTTCGCG TACTAATGAT CATGAATACA GGCTCCGCCT CTTATGGCTC
GCGCGCTAGA AGATGGAAAC TTTAATGAGC TCGCAGATGC GAGGCTTGAA GGCAACTACA
ACCCGCAAGA AATGGCTCGA ATGGTGAATT GTGCCGCTGC TAGCATTGTC CATTGGGGC
GTAAACGTCC AAAGATGAGC CAGGTGAATC AAAATTATAA CTAAAAGTCT ATTTTGTC
GAGAATAACA AACAAATGTT GTGGTTTCA GATAGTAAGA GCGTTAGAAG GAGAAGTGT
CTTAGATGCT TTAAACGAAG GTGTGAAGCC AGGACACAGT AACGTTTACG GGTCAATTGGG
AGCAAGCTCG GATTATAGTC AGACATCTA CAATGCAGAC ATGAAGAAAT TCAGACAGAT
AGCTTGTCG AGCCAAGAAT TCCCAGTCAG TGACTGTGAA GGAACATCTA GTAATGATT
TAGAGATATG GGAACTAAGA GCCCTACTCC TCCAAAATGA GATCGAATCA ATGATTCTGT

FIG. 12A(2)

1	M	A	S	S	P	E	S	A	P	P	T	N	S	T	S	S	P	S	P	P	20
1	ATG	GCT	TCT	TCT	CCT	GAA	TCT	GCT	CCT	CCA	ACA	AAC	TCC	ACC	TCT	TCT	CCA	TCT	CCA	CCG	60
21	S	N	T	N	S	T	T	S	S	P	P	A	P	S	P	P	S	P	T	P	40
61	TCT	AAT	ACC	AAT	TCA	ACC	ACC	TCT	TCT	CCG	CCG	GCT	CCG	TCT	CCT	CCT	TCT	CCT	ACA	CCT	120
41	P	Q	G	D	S	S	S	S	P	P	P	D	S	T	S	P	P	A	P	Q	60
121	CCT	CAA	GGA	GAC	TCA	TCA	TCA	TCG	CCA	CCT	CCT	GAT	TCC	ACA	TCT	CCA	CCA	GCT	CCA	CAA	180
61	A	P	N	P	P	N	S	S	N	N	S	P	S	P	P	S	Q	G	G	G	80
181	GCT	CCT	AAC	CCT	AAT	TCC	TCT	AAT	AAC	TCT	CCT	TCC	CCT	CCG	TCA	CAG	GGC	GGT	GGA	240	
81	G	E	R	G	N	G	G	N	N	G	G	N	D	T	P	P	S	R	G	S	100
241	GGA	GAA	AGA	GGA	AAT	GGA	GGA	AAC	AAT	GGT	GGC	AAT	GAT	ACT	CCA	CCG	TCA	CGC	GGC	TCT	300
101	P	P	S	P	P	S	R	S	N	G	D	N	G	G	S	R	S	S	P	P	120
301	CCT	CCT	TCT	CCT	TCT	AGG	AGT	AAT	GGA	GAT	AAT	GGT	GGT	AGC	AGA	TCA	TCG	CCA	CCA	360	
121	G	D	T	G	G	S	R	S	D	N	P	P	S	S	G	G	S	S	G	G	140
361	GGA	GAC	ACT	GGA	GGC	TCT	CGC	TCA	GAC	AAC	CCT	CCT	TCT	AGC	GGA	GGA	AGC	AGT	GGA	GGA	420
141	G	G	G	G	R	S	N	T	N	T	A	I	I	V	G	V	L	V	G	A	160
421	GGT	GGA	GGT	GGA	AGA	AGT	AAT	ACG	AAT	ACA	GCG	ATC	ATA	GTT	GGT	GTA	TTA	GTC	GGA	GCT	480
161	G	L	L	M	I	V	L	I	I	V	C	L	R	R	K	K	K	R	K	D	180
481	GGA	CTT	TTG	ATG	ATC	GTT	CTT	ATT	ATT	GTG	TGT	CTT	AGA	CGC	AAA	AAG	AAG	AGA	AAA	GAC	540
181	S	F	Y	P	E	P	M	K	G	N	Q	Y	Q	Y	Y	G	N	N	N	N	200
541	TCC	TTC	TAC	CCT	GAA	CCC	ATG	AAA	GGA	AAC	CAA	TAT	CAA	TAC	TAT	GGA	AAC	AAC	AAC	AAC	600
201	N	N	A	S	Q	N	Y	P	N	W	H	L	N	S	Q	G	Q	N	Q	Q	220
601	AAC	AAT	GCT	TCA	CAG	AAT	TAT	CCG	AAT	TGG	CAC	CTA	ATA	TCA	CAA	GGC	CAA	AAC	CAA	CAA	660
221	S	T	G	G	W	G	G	G	P	S	P	P	P	P	P	P	R	M	P	T	240
661	TCT	ACT	GGT	GGT	TGG	GGA	CGC	GGT	GGA	CCA	TCA	CCG	CCT	CCT	CCT	CCG	CGG	ATG	CCT	ACA	720
241	S	G	E	D	S	S	M	Y	S	G	P	S	R	P	V	L	P	P	P	S	260
721	AGC	GGA	GAA	GAT	TCT	TCC	ATG	TAC	TCA	GGC	CCA	TCA	CGC	CCA	GTT	TTA	CCT	CCT	CCT	TCG	780
261	P	A	L	A	L	G	F	N	K	S	T	F	T	Y	Q	E	L	A	A	A	280
781	CCT	GCT	CTA	GCC	CTC	GGA	TTC	AAC	AAG	AGC	ACT	TTT	ACT	TAC	CAA	GAG	CTT	GCG	GCT	GCA	840
281	T	G	G	F	T	D	A	N	L	L	G	Q	G	F	G	Y	V	H	K	300	
841	ACA	GGA	GGG	TTT	ACG	GAT	GCT	AAC	CTT	TTG	GGA	CAG	GGA	GGA	TTT	GGG	TAT	GTC	CAT	AAA	900
301	G	V	L	P	S	G	K	E	V	A	V	K	S	L	K	A	G	S	G	Q	320
901	GGA	GTC	TTG	CCT	AGC	GGG	AAA	GAA	GTA	GCA	GTT	AAG	AGT	TTA	AAA	GCG	GGT	AGC	GGA	CAA	960
321	G	E	R	E	F	Q	A	E	V	D	I	I	S	R	V	H	H	R	Y	L	340
961	GGA	GAG	AGG	GAG	TTT	CAA	GCT	GAG	GTC	GAT	ATC	ATT	AGC	CGT	GTG	CAT	CAT	CGG	TAT	CTT	1020
341	V	S	L	V	G	Y	C	I	A	D	G	Q	R	M	L	V	Y	E	F	V	360
1021	GTT	TCT	TTG	GTT	GGA	TAT	TGC	ATA	GCT	GAT	GGA	CAG	AGG	ATG	TTG	GTT	TAT	GAG	TTT	GTT	1080
361	P	N	K	T	L	E	Y	H	L	H	G	K	N	L	P	V	M	E	F	S	380
1081	CCT	AAC	AAA	ACT	TTG	GAA	TAT	CAT	CTT	CAT	GGG	AAA	AAT	CTT	CCG	GTA	ATG	GAG	TTC	TCC	1140
381	T	R	L	R	I	A	L	G	A	A	K	G	L	A	Y	L	H	E	D	C	400
1141	ACT	AGG	TTG	CGT	ATC	GCC	TTA	GGT	GCT	GCG	AAA	GGA	CTC	GCT	TAC	CTT	CAC	GAA	GAC	TGC	1200
401	H	P	R	I	I	H	R	D	I	K	S	A	N	I	L	L	D	F	N	F	420
1201	CAT	CCT	CGG	ATC	ATT	CAC	CGC	GAC	ATC	AAG	TCT	GCA	AAT	ATT	CTC	TTG	GAC	TTC	AAC	TTT	1260
421	D	A	M	V	A	D	F	G	L	A	K	L	T	S	D	N	N	T	H	V	440
1261	GAT	GCT	ATG	GTG	GCT	GAT	TTT	GGA	TTA	GCT	AAG	TTA	ACA	TCT	GAT	AAAC	AAAC	ACT	CAT	GTA	1320
441	S	T	R	V	M	G	T	F	G	Y	L	A	P	E	Y	A	S	S	G	K	460
1321	TCT	ACT	CGT	GTG	ATG	GGA	ACT	TTC	GGA	TAT	CTA	GCT	CCA	GAA	TAT	GCT	TCA	AGC	GGT	AAA	1380
461	L	T	E	K	S	D	V	F	S	Y	G	V	M	L	L	E	L	I	T	G	480
1381	TTA	ACC	GAG	AAA	TCC	GAT	GTT	TTC	TCT	TAC	GGA	GTT	ATG	TTA	TTG	GAA	CTT	ATA	ACT	GGA	1440
481	K	R	P	V	D	N	S	I	T	M	D	D	T	L	V	D	W	A	R	P	500
1441	AAA	CGA	CCG	GTT	GAT	AAT	AGC	ATC	ACC	ATG	GAC	GAC	ACC	TTA	GTA	GAT	TGG	GCT	CGG	CCT	1500

FIG. 12B(1)

501	L	M	A	R	A	L	E	D	G	N	F	N	E	L	A	D	A	R	L	E	520
1501	CTT	ATG	GCT	CGC	CGC	CTA	GAA	GAT	GGA	AAC	TTT	AAT	GAG	CTC	GCA	GAT	GCG	AGG	CTT	GAA	1560
521	G	N	Y	N	P	Q	E	M	A	R	M	V	T	C	A	A	A	S	I	R	540
1561	GGC	AAC	TAC	AAC	CCG	CAA	GAA	ATG	GCT	CGA	ATG	GTG	ACT	TGT	GCC	GCT	GCT	AGC	ATT	CGT	1620
541	H	S	G	R	K	R	P	K	M	S	Q	I	V	R	A	L	E	G	E	V	560
1621	CAT	TCG	GGG	CGT	AAA	CGT	CCA	AAG	ATG	AGC	CAG	ATA	GTA	AGA	GCG	TTA	GAA	GGA	GAA	GTG	1680
561	S	L	D	A	L	N	E	G	V	K	P	G	H	S	N	V	Y	G	S	L	580
1681	TCC	TTA	GAT	GCT	TTA	AAC	GAA	GGT	GTG	AAG	CCA	CGA	CAC	AGT	AAC	GTT	TAC	GGG	TCA	TTG	1740
581	G	A	S	S	D	Y	S	Q	T	S	Y	N	A	D	M	K	K	F	R	Q	600
1741	GGA	GCA	AGC	TCG	GAT	TAT	AGT	CAG	ACA	TCT	TAC	AAT	GCA	GAC	ATG	AAG	AAA	TTC	AGA	CAG	1800
601	I	A	L	S	S	Q	E	F	P	V	S	D	C	E	G	T	S	S	N	D	620
1801	ATA	GCT	TTG	TCG	AGC	CAA	GAA	TTC	CCA	GTC	AGT	GAC	TGT	GAA	GGA	ACA	TCT	AGT	AAT	GAT	1860
621	S	R	D	M	G	T	K	S	P	T	P	P	K	*							634
1861	TCT	AGA	GAT	ATG	GGA	ACT	AAG	AGC	CCT	ACT	CCT	CCA	AAA	TGA							1902

FIG. 12B(2)

TCCACCGTTT GAGAAACCTT AATAACAACA TTCAAAATGG CGGACTCACC GGTGGATTCA
TCTCCTGCCCT CTGAAACCTC AAATGGGACA CCACCGTCAA ACGGAACATC GCCGTCTAAT
GAGTCATCGC CGCCAACACC ACCTTCTTCA CCACCCACCAT CATCAATATC TGCTCCTCCG
CCAGATATCT CCGCTTCTTT TTCACCGCCG CCTGCACCAC CAACGCAAGA AACGTCACCT
CCTACATCTC CGTCCTCATC GCCGCCTGTT GTAGCTAATC CGTCACCGCA GACTCCAGAG
AATCCTTCTC CACCTGCACC TGAAGGCTCA ACTCCTGTAA CGCCACCTGC ACCACCACAA
ACACCGTCGA ACCAATCACC GGAAAGACCA ACTCCTCCTT CTCCTGGTGC CAATGATGAC
CGAAACAGAA CCAATGGCGG AAACAACAAC AGAGACGGCT CCACACCATC ACCACCGTCG
TCAGGGAAACA GAACTTCCGG TGACGGTGGC TCACCTTCAC CACCTCGGTC GATAAGCCCT
CCTCAGAATA GTGGAGATTG AGACTCATCA TCGGGTAATC ATCCACAAGC CAACATTGGA
TTGATTATTG GAGTCCTTGT AGGAGCAGGG CTTTGCTTC TACTTGCAGT GTGTATTTGC
ATCTGTTGCA ACAGGAAGAA GAAGAAGAAA TCTCCTCAGG TCAACCACAT GCACTACTAC
AATAACAATC CTTATGGAGG AGCACCCCTCA GGTAAATTACA GTTTAGTATA ACTGGAATT
AATTTGTAGC CTAATGGTGT TTGATTAGGT TTCAGAACGA TCATAGTCTA ATGGTTCTG
CTAGCTCCAT ATGGCAAAAG GATTAGATT ATAAGCTAAA GGAGATGTTG CATACTGTAG
GTAATGGTGG TTATTACAAG GGAACACCTC AAGATCATGT GGTGAATATG GCTGGTCAAG
GAGGTGGAA TTGGGGTCCA CAGCAACCTG TGTCTGGTCC TCACAGTGAT GCTTCCAAC
TAACCGGTG AACTGCTATA CCGTCACCTC AAGCTGCAAC TCTTGGTCAC AACCAAAGCA
CTTTCACATA CGATGAACTG TCCATTGCAA CAGAAGGTTT CGCTCAGTCA AATTTGCTAG
GACAAGGAGG ATTTGGGTAT GTTCATAAAG GAGTTCTGCC TAGTGGCAA GAAGTTGCAG
TGAAGAGTCT TAAACTTGGG AGTGGACAAG GGGAACGCGA GTTTCAAGCA GAGGTTGATA
TCATTAGCCG TGTCCATCAT CGTCATCTCG TTTCTTTGT TGGATATTGC ATCTCTCGT
GTCAAAGACT TTTGGTTTAT GAGTTTATAC CTAACAACAC TCTTGAATTT CATCTTCATG
GTACATTCCAT CTAACAGAAT GTTTCTTGT ATTAACAAAA CCTTTAAGTA TGGTTTCTCT

FIG. 13A(1)

TTAATCAGGA ACATGATTGA AATTCAGGA AAGGGTCGTC CGGTTTGGA TTGGCCTACA
AGAGTGAAGA TTGCATTGGG ATCAGCTAGA GCCCTGCAT ATTCGCATGA AGACTGTAAG
AAAATCTTA TCTCACATAT TTGCATCACT TTCTATCTCG CTCTCTACAA TATTGAAAG
ATTGTATATG TTACATCAAT TATAGGTAC CCTCGCATT TCCACAGAGA TATCAAAGCT
GCAAACATTC TTCTTGATTT CAGTTTGAG ACCAAGGTAT GTGTGTATAT ATCGACTCTT
GTACTACTTT TACTTCATT GTCTCTCATT TTTGTTCCA ATCTGTGTCG ATGTGTGTAT
CAGTCTTATT GTGAAATAT ATGCAGGTGG CAGATTGGA ATTGGCTAAG CTATCTCAAG
ACAACTATAC TCATGTCTCC ACTCGCGTCA TGGGAACCTT TGGGTAAGCA GCTTTGTAAA
ATGTCTAAC TCATCCACAC TTATTTAGTT TCTTCACTT GTTTTAACCA TTTTCTTGGA
TTCAGATACT TAGCTCCAGA GTATGCATCA AGCGGAAAGT TATCCGACAA ATCTGATGTT
TTCTCATTG GAGTAATGCT TCTTGAGCTC ATAACCGGAA GACCTCCTCT GGATCTAACT
GGAGAAATGG AAGATAGCTT GGTAGATTGG GTAAGTCGGT CCCCCCCTCT TCGGTTACT
TGTAAATCC CAAAACACTT TCCAAAGCAA AAACAGAAAC AAATCTTACT ATTGTTGTTG
CAGGCAAGGC CTTTGTGTT GAAAGCAGCT CAAGATGGAG ATTACAACCA ATTGGCTGAT
CCACGTCTAG AGCTAAACTA CAGTCATCAA GAGATGGTTC AAATGGCTTC TTGTCAGCT
GCAGCAATCA GACATTCAAGC AAGAAGACGG CCTAAGATGA GCCAGGTTCA AAAACTCATA
CCACTTGTG TTCTATTGT TATATTTTA CTCACAATT AATGATGAC TAAATGTGAC
ATACTAATGA ATCTGAAAC ATGTGTATGG TAAATGAAAA GATTGTACGA GCACTAGAAAG
GAGATATGTC AATGGATGAT CTAAGTGAGG GAACAAGACC AGGACAAAGC ACGTACTTGA
GCCCGGGAG CGTGAGCTCA GAGTATGACG CAAGCTCGTA CACGGCAGAC ATGAAAAAGT
TCAAGAAACT GGCAGTTAGAG AATAAAGAAT ATCAAAGCAG TGAATATGGT GGAACAAGTG
AGTATGGCTT AAACCCCTCT GCTTCAGTA GTGAAGAAAT GAATAGAGGC TCAATGAAAC
GCAATCCTCA GCTTTGAAAG AAGAGACAAC ACTTGTACATA ATATTCAGT TTTCTTCTCT

FIG. 13A(2)

1	M	A	D	S	P	V	D	S	S	P	A	P	E	T	S	N	G	T	P	P	20	
1	ATG	GCG	GAC	TCA	CCG	GTG	GAT	TCA	TCT	CCT	GCC	CCT	GAA	ACC	TCA	AAT	GGG	ACA	CCA	CCG	60	
21	S	N	G	T	S	P	S	N	E	S	S	P	P	T	P	P	S	S	P	P	40	
61	TCA	AAC	GGA	ACA	TCG	CCG	TCT	AAT	GAG	TCA	TCG	CCG	CCA	ACA	CCA	CCT	TCT	TCA	CCA	CCA	120	
41	P	S	S	I	S	A	P	P	P	D	I	S	A	S	F	S	P	P	P	A	60	
121	CCA	TCA	TCA	ATA	TCT	GCT	CCT	CCG	CCA	GAT	ATC	TCC	GCT	TCT	TTT	TCA	CCG	CCG	CCT	CCA	180	
61	P	P	T	Q	E	T	S	P	P	T	S	P	S	S	S	P	P	V	V	A	80	
181	CCA	CCA	ACG	CAA	GAA	ACG	TCA	CCT	CCT	ACA	TCT	CCG	TCC	TCA	TCG	CCG	CCT	GTT	GTA	GCT	240	
81	N	P	S	P	Q	T	P	E	N	P	S	P	P	A	P	E	G	S	T	P	100	
241	AAT	CCG	TCA	CCG	CAG	ACT	CCA	GAG	AAT	CCT	TCT	CCA	CCT	GCA	CCT	GAA	GGC	TCA	ACT	CCT	300	
101	V	T	P	P	A	P	P	Q	T	P	S	N	Q	S	P	E	R	P	T	P	120	
301	GTA	ACG	CCA	CCT	GCA	CCA	CCA	CAA	ACA	CCG	TCG	AAC	CAA	TCA	CCG	GAA	AGA	CCA	ACT	CCT	360	
121	P	S	P	G	A	N	D	D	R	N	R	T	N	G	G	N	N	N	R	D	140	
361	CCT	TCT	CCT	GGT	GCC	AAT	GAT	GAC	CGA	AAC	AGA	ACC	AAT	GGC	GGA	AAC	AAC	AAC	AGA	GAC	420	
141	G	S	T	P	S	P	P	S	S	G	N	R	T	S	G	D	G	G	S	P	160	
421	GGC	TCC	ACA	CCA	TCA	CCA	CCG	TCG	TCA	GGG	AAC	AGA	ACT	TCC	GGT	GAC	GGT	GGC	TCA	CCT	480	
161	S	P	P	R	S	I	S	P	P	Q	N	S	G	D	S	D	S	S	S	G	180	
481	TCA	CCA	CCT	CGG	TCG	ATA	AGC	CCT	CCT	CAG	AAT	AGT	GGG	GAT	TCA	GAC	TCA	TCA	TCG	GGG	540	
181	L	L	L	L	A	V	C	I	C	I	C	C	C	N	R	K	K	K	K	K	200	
541	CTT	TTG	CTT	CTA	CTT	GCA	GTG	TGT	ATT	TGC	ATC	TGT	TGC	AAC	AGG	AAG	AAG	AAG	AAG	AAA	600	
201	S	P	Q	V	N	H	M	H	Y	Y	N	N	N	P	Y	G	G	A	P	S	220	
601	TCT	CCT	CAG	GTC	AAC	CAC	ATG	CAC	TAC	TAC	AAT	AAC	AAT	CCT	TAT	GGG	GGG	GCA	CCC	TCA	660	
221	G	N	G	G	Y	Y	K	G	T	P	Q	D	H	V	V	N	M	A	G	Q	240	
661	GGT	AAT	GGT	GGT	TAT	TAC	AAG	GGG	ACA	CCT	CAA	GAT	CAT	GTG	GTG	GTG	AAT	ATG	GCT	GGT	CAA	720
241	G	G	G	N	W	G	P	Q	Q	P	V	S	G	P	H	S	D	A	S	N	260	
721	GGA	GGT	GGG	AAT	TGG	GGT	CCA	CAG	CAA	CCT	GTG	TCT	GGT	CCT	CAC	AGT	GAT	GCT	TCC	AAC	780	
261	L	T	G	R	T	A	I	P	S	P	Q	A	A	T	L	G	H	N	Q	S	280	
781	TTA	ACC	GGT	CGA	ACT	GCT	ATA	CCG	TCA	CCT	CAA	GCT	GCA	ACT	CTT	GGT	CAC	AAC	CAA	AGC	840	
281	T	F	T	Y	D	E	L	S	I	A	T	E	G	F	A	Q	S	N	L	L	300	
841	ACT	TTC	ACA	TAC	GAT	GAA	CTG	TCC	ATT	GCA	ACA	GAA	GGT	TTC	GCT	CAG	TCA	AAT	TTG	CTA	900	
301	G	Q	G	G	F	G	Y	V	H	K	G	V	L	P	S	G	K	E	V	A	320	
901	GGA	CAA	GGA	GGA	TTT	GGG	TAT	GTT	CAT	AAA	GGG	GTT	CTG	CCT	AGT	GGC	AAA	GAA	GTT	GCA	960	
321	V	K	S	L	K	L	G	S	G	Q	G	E	R	E	F	Q	A	E	V	D	340	
961	GTG	AAG	AGT	CTT	AAA	CTT	GGA	AGT	GGA	CAA	GGG	GAA	CGC	GAG	TTT	CAA	GCA	GAG	GTT	GAT	1020	
341	I	I	S	R	V	H	H	R	H	L	V	S	L	V	G	Y	C	I	S	G	360	
1021	ATC	ATT	AGC	CGT	GTC	CAT	CAT	CGT	CAT	CTC	GTT	TCT	CTT	GTT	GGA	TAT	TGC	ATC	TCT	GGT	1080	
361	G	Q	R	L	L	V	Y	E	F	I	P	N	N	T	L	E	F	H	L	H	380	
1081	GGT	CAA	AGA	CTT	TTG	GTT	TAT	GAG	TTT	ATA	CCT	AAC	ACT	CTT	GAA	TTT	CAT	CTT	CAT	1140		
381	G	K	G	R	P	V	L	D	W	P	T	R	V	K	I	A	L	G	S	A	400	
1141	GGA	AAG	GGT	CGT	CCG	GTT	TTG	GAT	TGG	CCT	ACA	AGA	GTG	AAG	ATT	GCA	TTG	GGA	TCA	GCT	1200	
401	R	G	L	A	Y	L	H	E	D	C	K	K	I	F	I	S	H	I	C	I	420	
1201	AGA	GGC	CTT	GCA	TAT	TTG	CAT	GAA	GAC	TGT	AAG	AAA	ATC	TTT	ATC	TCA	CAT	ATT	TGC	ATC	1260	
421	S	H	P	R	I	I	H	R	D	I	K	A	A	N	I	L	L	D	F	S	440	
1261	AGT	CAC	CCT	CGC	ATT	ATC	CAC	AGA	GAT	ATC	AAA	GCT	GCA	AAC	ATT	CTT	CTT	GAT	TTC	AGT	1320	
441	F	E	T	K	V	A	D	F	G	L	A	K	L	S	Q	D	N	Y	T	H	460	
1321	TTT	GAG	ACC	AAG	GTC	GCA	GAT	TTT	GGA	TTG	GCT	AAG	CTA	TCT	CAA	GAC	AAC	TAT	ACT	CAT	1380	
461	V	S	T	R	V	M	G	T	F	G	Y	L	A	P	E	Y	A	S	S	G	480	
1381	GTC	TCC	ACT	CGC	GTC	ATG	GGA	ACT	TTT	GGA	TAC	TTA	GCT	CCA	GAG	TAT	GCA	TCA	AGC	GGG	1440	
481	K	L	S	D	K	S	D	V	F	S	F	G	V	M	L	L	E	L	I	T	500	
1441	AAG	TTA	TCC	GAC	AAA	TCT	GAT	GTT	TTC	TCA	TTT	GGA	GTA	ATG	CTT	CTT	GAG	CTC	ATA	ACC	1500	
501	G	R	P	P	L	D	L	T	G	E	M	E	D	S	L	V	D	W	A	R	520	
1501	GGA	AGA	CCT	CCT	CTG	GAT	CTA	ACT	GGA	GAA	ATG	GCA	AGC	TTG	GTA	GAT	TGG	GCA	AGG	1560		

FIG. 13B(1)

521	P	L	C	L	K	A	A	Q	D	G	D	Y	N	Q	L	A	D	P	R	L	540
1561	CCT	TTG	TGT	TTG	AAA	GCA	GCT	CAA	GAT	GGA	GAT	TAC	AAC	CAA	TTG	GCT	GAT	CCA	CGT	CTA	1620
541	E	L	N	Y	S	H	Q	E	M	V	Q	M	A	S	C	A	A	A	A	I	560
1621	GAG	CTA	AAC	TAC	AGT	CAT	CAA	GAG	ATG	GTT	CAA	ATG	GCT	TCT	TGT	GCA	GCT	GCA	GCA	ATC	1680
561	R	H	S	A	R	R	R	P	K	M	S	Q	V	Q	K	L	I	P	L	V	580
1681	AGA	CAT	TCA	GCA	AGA	AGA	CGG	CCT	AAG	ATG	AGC	CAG	GTT	CAA	AAA	CTC	ATA	CCA	CTT	GTT	1740
581	G	S	I	I	V	R	A	L	E	G	D	M	S	M	D	D	L	S	E	G	600
1741	GGT	TCT	ATT	ATT	GTA	CGA	GCA	CTA	GAA	GGA	GAT	ATG	TCA	ATG	GAT	GAT	CTA	AGT	GAG	GGA	1800
601	T	R	P	G	Q	S	T	Y	L	S	P	G	S	V	S	S	E	Y	D	A	620
1801	ACA	AGA	CCA	GGA	CAA	AGC	ACC	TAC	TTG	AGC	CCC	GGG	AGC	GTC	AGC	TCA	GAG	TAT	GAC	GCA	1860
621	S	S	Y	T	A	D	M	K	K	F	K	K	L	A	L	E	N	K	E	Y	640
1861	AGC	TCG	TAC	ACG	GCA	GAC	ATG	AAA	AAG	TTC	AAG	AAA	CTG	GCG	TTA	GAG	AAT	AAA	GAA	TAT	1920
641	Q	S	S	E	Y	G	G	T	S	E	Y	G	L	N	P	S	A	S	S	S	660
1921	CAA	AGC	AGT	GAA	TAT	GGT	GGA	ACA	AGT	GAG	TAT	GGC	TTA	AAC	CCT	TCT	GCT	TCA	AGT	AGT	1980
661	E	E	M	N	R	G	S	M	K	R	N	P	Q	L	*						675
1981	GAA	GAA	ATG	AAT	AGA	GGC	TCA	ATG	AAA	CGC	AAT	CCT	CAG	CTT	TGA						2025

FIG. 13B(2)

CATAACATCAC AAAACGGCAT CGTTTGATG TCGCTCTCTC CTTCTTCCTC GCCGGCTCCG
GCAACTTCCC CGCCTGCCAT GTCATTACCT CCGGCAGATT CCGTACCTGA CACGTCATCA
CCTCCAGCTC CTCCCTTGTC TCCTCTTCCC CCACCATGTA GCTCTCCTCC GCCGTTGCCT
TCACCAACCGC CTCTCTCCGC TCCCACCGCT TCCCCACCGC CTCTTCCGGT TGAATCCCCA
CCGTCTCCTC CTATAGAAC ACCACCCGCT CCTCTACTGG AATCACCTCC TCCTCCTCCG
TTGGAATCTC CATCTCCACC GTCTCCTCAC GTCTCAGCTC CTTCCGGTTC ACCGCCATTA
CCCTTCCTTC CCGCCAAACC TTCTCCGCCG CCTTCTTCAC CTCCCTCCGA GACAGTTCCG
CCGGGAAATA CGATTTCTCC ACCACCTCGT TCACTCCCT CCGAATCAAC CCCGCCGGTG
AACACAGCTT CTCCCTCCACC GCCATCTCCT CCTCGCCGCC GTAGTGGCCC TAAGCCTTCG
TTTCCCTCCTC CCATCAATTTC TTCTCCACCA AATCCTTCTC CGAACACTCC GTCACTCCCA
GAAACTTCTC CTCCACCTAA ACCACCCGCTC TCAACGACGC CATTTCCTC CTCATCCACT
CCCCCGCCTA AGAAGTCCCC TGCAGCAGTA ACTCTTCCTT TCTTGGGCC AGCGGGCAA
TTACCGGATG GGACCGTAGC ACCTCCTATT GGGCCTGTTA TAGAGCCAA GACGAGTCCA
GCCGAATCAA TATCTCCGGG AACGCCACAG CCACTGGTTC CGAAGAGTCT ACCTGTAACG
ACGTCGTATC ACCGATCATC CGCCGGATTC TTATTTGGCG GTGTAATCGT TGGAGCTCTT
CTACTAATTTC TGTTAGGTCT TCTCTTGTC TTCTACAGAG CTACAGAAA TAGAAATAAC
AACAGCAGCT CTGCTCATCA TCAATCCAAA ACTCCCTCAA AAGGTATAAA CTTTGAGATC
AATTTGTTTC AGACTGTCAC TTAAAATGTA ATGTAATTGT AAGTTATGAT CTTTTTGCT
TGGATCAGTT CAAACATCATC GGGCGGTAA TGCTGGTACG AACCAGGCAC ATGTTATCAC
AATGCCACCA CCAATCCATG CTAAATATAT ATCTAGTGGA GGTGTCATA CGAAGGAGAA
CAATTCTGTT GCGAAAAAACCA TTTCAATGCC ATCTGGAATG TTCTCCTACG AAGAACTTTC
AAAAGCAACT GGTGGATTTT CAGAGGAGAA CCTTTGGGA GAAGGCGGTT TCGGATATGT
TCACAAAGGA GTGTTGAAAA ACGGGACAGA AGTTGCGGTG AAGCAGCTGA AGATTGGGAG
CTATCAAGGG GAAAGAGAAT TCCAAGCTGA GGTTGACACA ATCAGTAGGG TTCATCATAA
GCACCTCGTT TCATTGGTTG GTTATTGCGT TAATGGAGAT AAAAGACTCT TGGTTACGA
GTTTGTTCCT AAAGATAACCT TGGAGTTCCA CTTGCATGGT AAAATAGATA TATGATTTCA

FIG. 14A(1)

TCCTTTGA TTTTGTCTT AGTCATTAT GTTGAGTATT GTGAGAATAT GTGTTGAGA
GAACAGAGGA AGCGTGTGG AATGGAAAT GAGGCTCAGG ATTGCTGTAG GAGCAGCAA
AGGATTAGCT TATCTTCATG AGGATTGTGA GTTGTTCCTC TTCATAATGG GAATGACAAT
GGCCTTTTT GGGTTTCGA CACTGATATT GATTCTGGT GCTTGTAAATG CAGGCAGTCC
AACTATAATT CACCGTGATA TCAAAGCAGC TAATATCCTT CTAGAATCCA AATTGAGGC
AAAGGTGATC TGCTCTTAA TCTTATCAA GTTTGGTTTT TAGAACAGAG TTTGCCATT
TTCGGTTTAT AGTCACACCCA TTTTGTCTA TTTAACAAAGA TTACATGTAG CTTAGAGTTC
TTGTTCTCTT CAGGTCTCTG ACTTTGGACT AGCCAAGTTT TTCTCAGACA CCAATTCCATC
ATTCACTCAT ATCTCTACTC GAGTGGTAGG AACTTCGGG TAAAACACCA TCCATCCATG
CTTTATATGT TGTGTCATTG TGTTTAAAAA TATTAATTAA CGGTTTCAAG TTTCAAGTTT
CAAGTTCAA GTTTCTTCCT TGTTGTATCG TAAATCCAGA TCAAAAGATT TATTGATTAC
TAAATGCCTT GTGCACCGTC TATTTGGTAT GCATTTAAC AGATACATGG CTCCAGAATA
CGCGTCCAGT GGTAAAGTAA CTGATAAAC AGATGTATAT CCCTTGGGG TCGTGCTTCT
AGAAACTCATC ACTGGACGTC CATCAATTTC CGCCAAAGAT TCTTCCACAA ACCAGAGTTT
AGTAGACTGG GTAAGTCAAA GTACATGATG ATGATGATGA TACCATTAAGG TTTCTTTTT
CCCACTAGTT ATTAGATGAA AATGAAACTC CAGTATAACT GCAAGCTTGA AACTTCATTA
GAAGTAAAT TTTGATTATT CCTCAGGCGA GGCCATTGCT TACGAAAGCA ATCTCTGAAG
AAAGTTTGA CTTTCTTGTAA GACTCAAGGT TGAGAAGAA TTACGATACA ACTCAGATGG
CAAACATGGC TGCTTGTGCT GCTGCTTGA TACGCCAATC AGCTTGGCTT CGGCCTAGAA
TGAGGCCAGGT CTGAGATTAA GTTTAAATAC ATGTATTGCT CCATATATCC GAAAGGAACA
AGCCTAATCC ATGAATACAT TTATATCTTGA AAAAAAAACTT GAATAGGTAG TACGTGCTCT
TGAAGGCAG GTGGCCCTGA GAAAGCTGA AGAGACTGGG AATAGCGTGA CCTATAGCTC
TTCTGAAAAC CCGAATGACA TCACACCACG GTATGGAACA AATAAGAGGA GATTGACAC
AGGTTCAAGC GATGGTTACA CTTCAGAATA TGAGTTAAC CCTTCTCAGT CGAGCAGTGA
ACATCAACAG GTGAATACTT AGTTCACAGG TTCAATAGGG CAAGTTTCAC CACAATTATT

FIG. 14A(2)

1	M	S	L	S	P	S	S	S	P	A	P	A	T	S	P	P	A	M	S	L	20	
1	ATG	TCG	CTC	TCT	CCT	TCT	TCC	TCG	CCG	GCT	CCG	GCA	ACT	TCC	CCG	CCT	GCC	ATG	TCA	TTA	60	
21	P	P	A	D	S	V	P	D	T	S	S	P	P	A	P	P	L	S	P	L	40	
61	CCT	CCG	GCA	GAT	TCC	GTA	CCT	GAC	ACG	TCA	TCA	CCT	CCA	GCT	CCT	CCT	TTG	TCT	CCT	CTT	120	
41	P	P	P	L	S	S	P	P	P	L	P	S	P	P	P	L	S	A	P	T	60	
121	CCC	CCA	CCA	TTG	AGC	TCT	CCT	CCG	CCG	TTG	CCT	TCA	CCA	CCG	CCT	CTC	TCC	GCT	CCC	ACC	180	
61	A	S	P	P	P	L	P	V	E	S	P	P	S	P	P	P	I	E	S	P	80	
181	GCT	TCC	CCA	CCG	CCT	CTT	CCG	GTT	GAA	TCC	CCA	CCG	TCT	CCT	CCT	ATA	GAA	TCA	CCA	CCG	240	
81	P	P	L	L	E	S	P	P	P	P	L	E	S	P	S	P	P	S	P	100		
241	CCT	CCT	CTA	CTG	GAA	TCA	CCT	CCT	CCT	CCG	TTG	GAA	TCT	CCA	TCT	CCA	CCG	TCT	CCT	300		
101	H	V	S	A	P	S	G	S	P	P	L	P	F	L	P	A	K	P	S	P	120	
301	CAC	GTC	TCA	GCT	CCT	TCC	GGT	TCA	CCG	CCA	TTA	CCC	TTC	CTT	CCC	GCC	AAA	CCT	TCT	CCG	360	
121	P	P	S	S	P	P	S	E	T	V	P	P	G	N	T	I	S	P	P	140		
361	CCG	CCT	TCT	TCA	CCT	CCC	TCC	GAG	ACA	GTT	CCG	CCG	GGA	AAT	ACG	ATT	TCT	CCA	CCA	CCT	420	
141	R	S	L	P	S	E	S	T	P	P	V	N	T	A	S	P	P	P	P	S	160	
421	CGT	TCA	CTT	CCC	TCC	GAA	TCA	ACC	CCG	CCG	GTC	AAC	ACA	GCT	TCT	CCT	CCA	CCG	CCA	TCT	480	
161	P	P	R	R	R	S	G	P	K	P	S	F	P	P	P	I	N	S	S	P	180	
481	CCT	CCT	CGC	CGC	CGT	AGT	GGC	CCT	AAG	CCT	TCG	TTT	CCT	CCT	CCC	ATC	AAT	TCT	TCT	CCA	540	
181	P	N	P	S	P	N	T	P	S	L	P	E	T	S	P	P	P	K	P	P	200	
541	CCA	AAT	CCT	TCT	CCG	AAC	ACT	CCG	TCA	CTC	CCA	GAA	ACT	TCT	CCT	CCA	CCT	AAA	CCA	CCG	600	
201	L	S	T	T	P	F	P	S	S	S	T	P	P	P	K	K	S	P	A	A	220	
601	CTC	TCA	ACG	ACG	CCA	TTT	CCC	TCC	TCA	TCC	ACT	CCC	CCG	CCT	AAG	AAG	TCC	CCT	GCA	GCA	660	
221	V	T	L	P	F	F	G	P	A	G	Q	L	P	D	G	T	V	A	P	P	240	
661	GTA	ACT	CTT	CCT	TTC	TTT	GGG	CCA	GGC	GGC	CAA	TTA	CCG	GAT	GGG	ACC	GTA	GCA	CCT	CCT	720	
241	I	G	P	V	I	E	P	K	T	S	P	A	E	S	I	S	P	G	T	P	260	
721	ATT	GGG	CCT	GTT	ATA	GAG	CCC	AAG	ACG	AGT	CCA	GCC	GAA	TCA	ATA	TCT	CCG	GGA	ACG	CCA	780	
261	Q	P	L	V	P	K	S	L	P	V	T	T	S	Y	H	R	S	S	A	G	280	
781	CAG	CCA	CTG	GTT	CCG	AAG	AGT	CTA	CCT	GTA	ACG	ACG	TCG	TAT	CAC	CGA	TCA	TCC	GCC	GGA	840	
281	F	L	F	G	G	V	I	V	G	A	L	L	I	L	L	G	L	L	F	300		
841	TTC	TTA	TTT	GGC	GGT	GTA	ATC	GTT	GGA	GCT	CTT	CTA	CTA	ATT	CTG	TTA	GGT	CTT	CTC	TTT	900	
301	V	F	Y	R	A	T	R	N	R	N	N	N	N	S	S	S	A	H	H	Q	S	320
901	GTC	TTC	TAC	AGA	GCT	ACC	AGA	AAT	AGA	AAT	AAC	AAC	AGC	AGC	TCT	GCT	CAT	CAT	CAA	TCC	960	
321	K	T	P	S	K	V	Q	H	H	R	G	G	N	A	G	T	N	Q	A	H	340	
961	AAA	ACT	CCC	TCA	AAA	GTT	CAA	CAT	CAT	CGG	GGC	GGT	AAT	GCT	GGT	ACG	AAC	CAG	GCA	CAT	1020	
341	V	I	T	M	P	P	P	I	H	A	K	Y	I	S	S	G	G	C	D	T	360	
1021	GTT	ATC	ACA	ATG	CCA	CCA	CCA	ATC	CAT	GCT	AAA	TAT	ATA	TCT	AGT	GGA	GGT	TGT	GAT	ACG	1080	
361	K	E	N	N	S	V	A	K	N	I	S	M	P	S	G	M	F	S	Y	E	380	
1081	AAG	GAG	AAC	AAT	TCT	GTT	GGC	AAA	AAC	ATT	TCA	ATG	CCA	TCT	GGA	ATG	TTC	TCC	TAC	GAA	1140	
381	E	L	S	K	A	T	G	G	F	S	E	E	N	L	L	G	E	G	G	F	400	
1141	GAA	CTT	TCA	AAA	GCA	ACT	GGT	GGG	TTT	TCA	GAG	GAG	AAC	CTT	TTG	GGA	GAA	GGC	GGT	TTC	1200	
401	G	Y	V	H	K	G	V	L	K	N	G	T	E	V	A	V	K	Q	L	K	420	
1201	GGA	TAT	GTT	CAC	AAA	GGG	GTG	TTG	AAA	AAC	GGG	ACA	GAA	GTT	GCG	GTG	AAG	CAG	CTG	AAG	1260	
421	I	G	S	Y	Q	G	E	R	E	F	Q	A	E	V	D	T	I	S	R	V	440	
1261	ATT	GGG	AGC	TAT	CAA	GGG	GAA	AGA	GAA	TTC	CAA	GCT	GAG	GTT	GAC	ACA	ATC	AGT	AGG	GTT	1320	
441	H	H	K	H	L	V	S	L	V	G	Y	C	V	N	G	D	K	R	L	L	460	
1321	CAT	CAT	AAG	CAC	CTC	GTT	TCA	TTG	GTT	GGT	TAT	TGC	GTT	AAT	GGA	CAT	AAA	AGA	CTC	TTG	1380	
461	V	Y	E	F	V	P	K	D	T	L	E	F	H	L	H	E	N	R	G	S	480	
1381	GTT	TAC	GAG	TTT	GTT	CCT	AAA	GAT	ACC	TTG	GAG	TTC	CAC	TTG	CAT	GAG	AAC	AGA	GGA	AGC	1440	
481	V	L	E	W	E	M	R	L	R	I	A	V	G	A	A	K	G	L	A	Y	500	
1441	GTG	TTG	GAA	TGG	GAA	ATG	AGG	CTC	AGG	ATT	GCT	GTA	GGA	GCA	GCA	AAA	GGA	TTA	GCT	TAT	1500	
501	L	H	E	D	C	S	P	T	I	I	H	R	D	I	K	A	A	N	I	L	520	

FIG. 14B(1)

1501	CTT	CAT	GAG	GAT	TGC	AGT	CCA	ACT	ATA	ATT	CAC	CGT	GAT	ATC	AAA	GCA	GCT	AAT	ATC	CTT	1560
521	L	D	S	K	F	E	A	K	V	S	D	F	G	L	A	K	F	F	S	D	540
1561	CTA	GAT	TCC	AAA	TTT	GAG	GCA	AAG	GTC	TCT	GAC	TTT	GGA	CTA	GCC	AAG	TTT	TTC	TCA	GAC	1620
541	T	N	S	S	F	T	H	I	S	T	R	V	V	G	T	F	G	Y	M	A	560
1621	ACC	AAT	TCA	TCA	TTC	ACT	CAT	ATC	TCT	ACT	CGA	GTG	GTA	GGA	ACT	TTC	GGA	TAC	ATG	GCT	1680
561	P	E	Y	A	S	S	G	K	V	T	D	K	S	D	V	Y	S	F	G	V	580
1681	CCA	GAA	TAC	GCG	TCC	AGT	GGT	AAA	GTA	ACT	GAT	AAA	TCA	GAT	GTA	TAT	TCC	TTT	GGG	GTC	1740
581	V	L	L	E	L	I	T	G	R	P	S	I	F	A	K	D	S	S	T	N	600
1741	G TG	CTT	CTA	GAA	CTC	ATC	ACT	GGA	CGT	CCA	TCA	ATT	TTC	GCC	AAA	GAT	TCT	TCC	ACA	AAC	1800
601	Q	S	L	V	D	W	A	R	P	L	L	T	K	A	I	S	G	E	S	F	620
1801	CAG	AGT	TTA	GTA	GAC	TGG	GCG	AGG	CCA	TTG	CTT	ACG	AAA	GCA	ATC	TCT	GGA	GAA	AGT	TTT	1860
621	D	F	L	V	D	S	R	L	E	K	N	Y	D	T	T	Q	M	A	N	M	640
1861	GAC	TTT	CTT	GTA	GAC	TCA	AGG	TTG	GAG	AAG	AAT	TAC	GAT	ACA	ACT	CAG	ATG	GCA	AAC	ATG	1920
641	A	A	C	A	A	A	C	I	R	Q	S	A	W	L	R	P	R	M	S	Q	660
1921	GCT	GCT	TGT	GCT	GCT	TGC	ATA	CGC	CAA	TCA	GCT	TGG	CTT	CGG	CCT	AGA	ATG	AGC	CAG	1980	
661	V	V	R	A	L	E	G	E	V	A	L	R	K	V	E	E	T	G	N	S	680
1981	GTA	GTA	CGT	GCT	CTT	GAA	GCG	GAG	GTG	GCC	CTG	AGA	AAG	GTC	GAA	GAG	ACT	GGG	AAT	AGC	2040
681	V	T	Y	S	S	S	E	N	P	N	D	I	T	P	R	Y	G	T	N	K	700
2041	G TG	ACC	TAT	AGC	TCT	TCT	GAA	AAC	CCG	AAT	GAC	ATC	ACA	CCA	CGG	TAT	CGA	ACA	AAT	AAG	2100
701	R	R	F	D	T	G	S	S	D	G	Y	T	S	E	Y	G	V	N	P	S	720
2101	AGG	AGA	TTC	GAC	ACA	GGT	TCA	AGC	GAT	GGT	TAC	ACT	TCA	GAA	TAT	GGA	GTT	AAC	CCT	TCT	2160
721	Q	S	S	S	E	H	Q	Q	V	N	T	*									732
2161	CAG	TCG	AGC	AGT	GAA	CAT	CAA	CAG	GTG	AAT	ACT	TAG									2196

FIG. 14B(2)

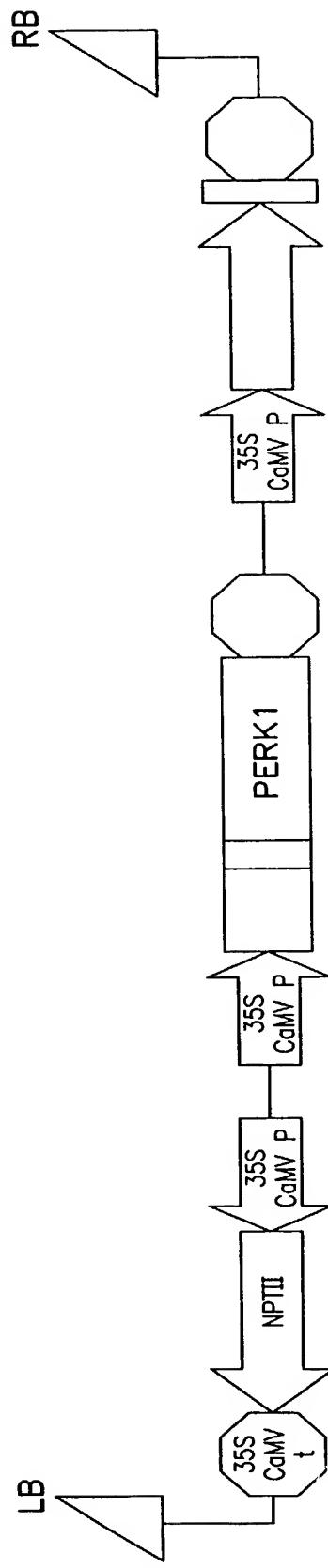


FIG. 15

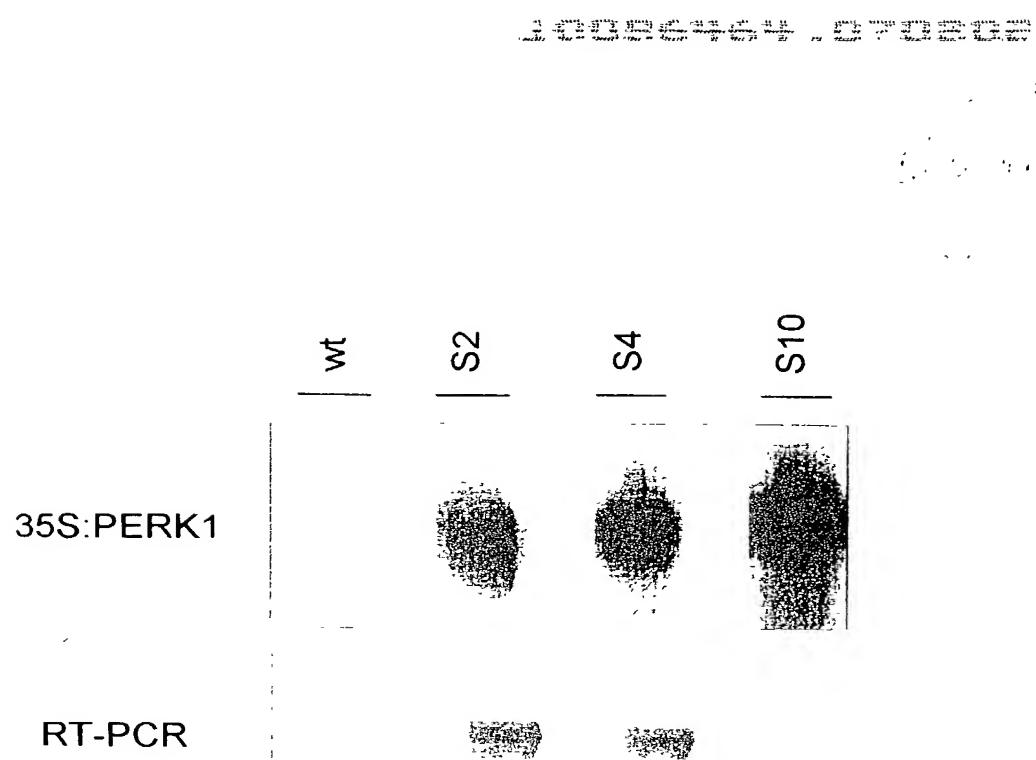


FIG. 16A

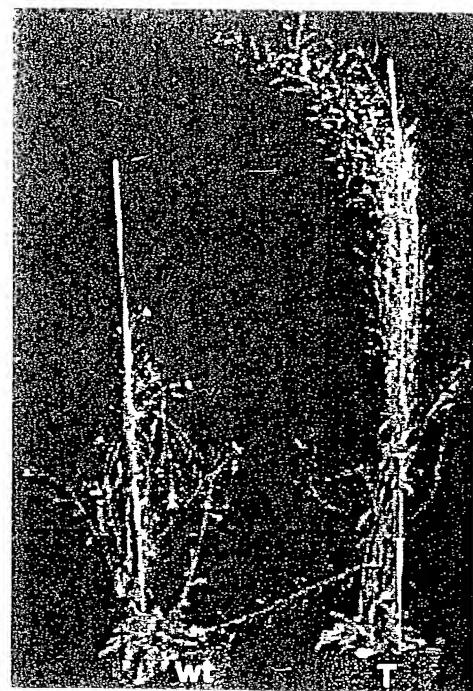


FIG. 16B

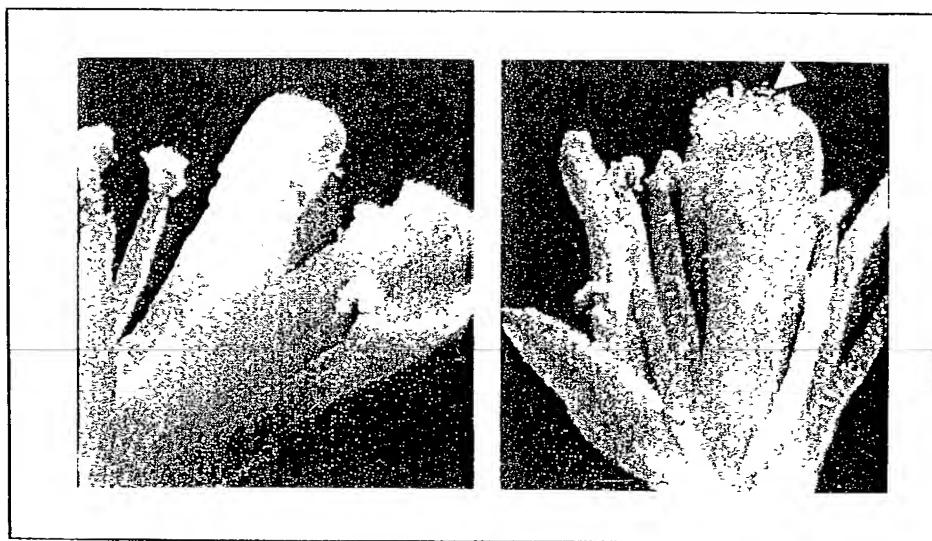


FIG. 17

	Wild-type	Overexpressing PERK1 Lines
Average seeds/silique	37	54
Average dry seed weight/plant	60.2 mg	106.2 mg

FIG. 18A

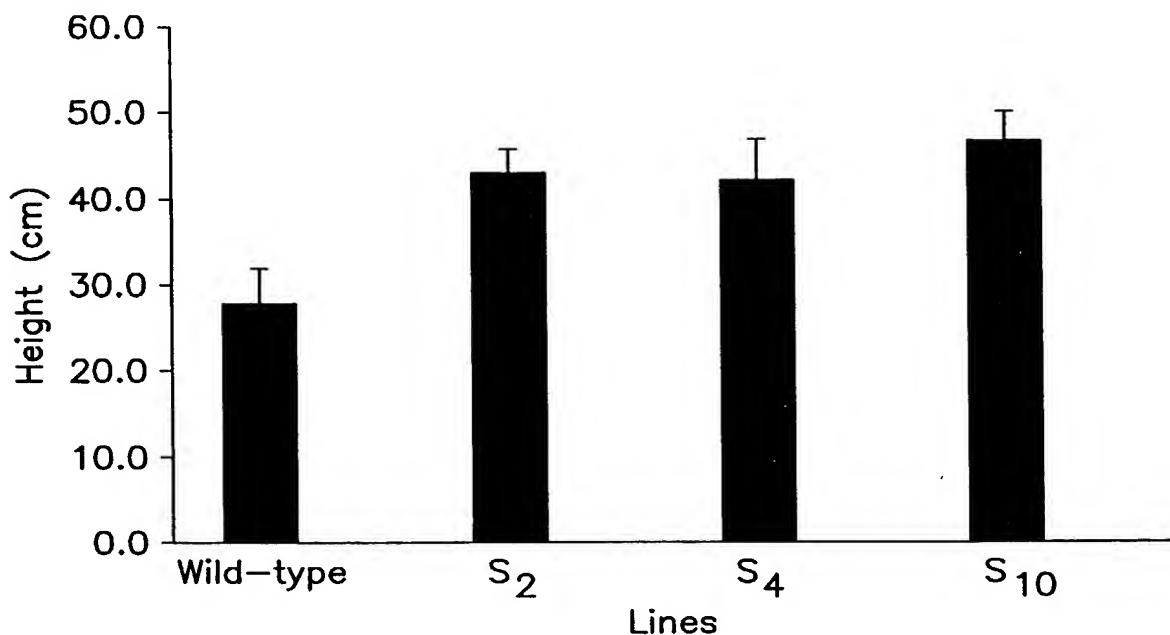


FIG. 18B

FIG. 19B

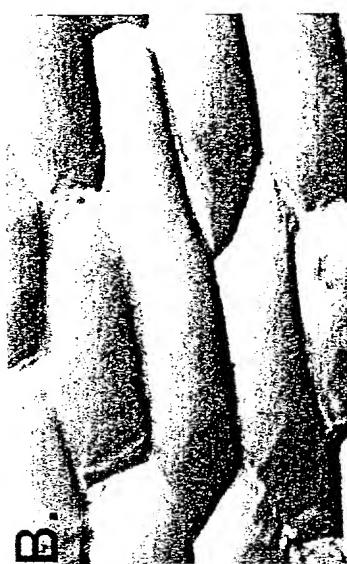


FIG. 19D



FIG. 19F



FIG. 19A



FIG. 19C

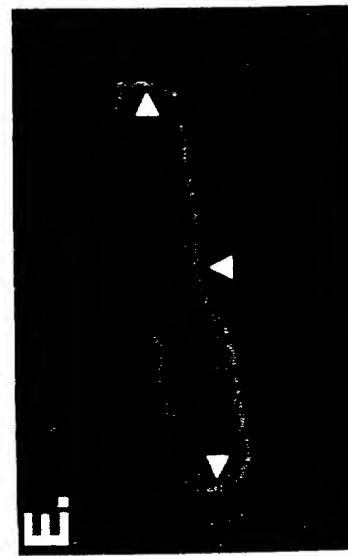


FIG. 19E